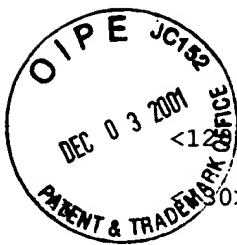


SEQUENCE LISTING



<110> Witman, George B.
Pazour, Gregory J.
Rosenbaum, Joel L.
Cole, Douglas G.

<120> INTRAFAGELLAR TRANSPORT

<130> 07917-145001

<140> US 09/866,582

<141> 2001-05-24

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gac gcg gta gat aga gga gtc tac ttt gac gag gac ttt cat gtc cgc 164
Asp Ala Val Asp Arg Gly Val Tyr Phe Asp Glu Asp Phe His Val Arg
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att ctt gat gtt gac aag tac aat gct tca aag tcg ctc cag gac aac 212
Ile Leu Asp Val Asp Lys Tyr Asn Ala Ser Lys Ser Leu Gln Asp Asn
20 25 30

aca aat gtg ttc att aac aac atc caa aat atg caa ggc ctc gtg gac 260
Thr Asn Val Phe Ile Asn Asn Ile Gln Asn Met Gln Gly Leu Val Asp
35 40 45

aag tac gtg tcc gcc atc gac cag cag gtc gag cgg cta gaa gct gaa 308
Lys Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg Leu Glu Ala Glu
50 55 60 65

aag ctg aag gcc att ggc ctg cgg aac cgg gtg gct gcg ctg agc gag 356
Lys Leu Lys Ala Ile Gly Leu Arg Asn Arg Val Ala Ala Leu Ser Glu
70 75 80

Sub
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 Glu Arg Lys Arg Lys Gln Lys Glu Gln Glu Arg Met Leu Ala Glu Lys
 85 90 95

cag gag gag ctt gag agg ctc caa atg gag gag cag tcg ctg atc aag 452
 Gln Glu Glu Leu Glu Arg Leu Gln Met Glu Glu Gln Ser Leu Ile Lys
 100 105 110

gtg aag ggc gag cag gag ctc atg att cag aag ctg tcg gac agc agc 500
 Val Lys Gly Glu Gln Glu Leu Met Ile Gln Lys Leu Ser Asp Ser Ser
 115 120 125

agc ggg gcg gca tac gtg taaacggtgt tcggacgtca tgcgtgcaaa 548
 Ser Gly Ala Ala Tyr Val
 130 135

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 35 40 45
 Asp Lys Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg Leu Glu Ala
 50 55 60
 Glu Lys Leu Lys Ala Ile Gly Leu Arg Asn Arg Val Ala Ala Leu Ser
 65 70 75 80
 Glu Glu Arg Lys Arg Lys Gln Lys Glu Gln Glu Arg Met Leu Ala Glu
 85 90 95
 Lys Gln Glu Glu Leu Glu Arg Leu Gln Met Glu Glu Gln Ser Leu Ile
 100 105 110
 Lys Val Lys Gly Glu Gln Glu Leu Met Ile Gln Lys Leu Ser Asp Ser
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 Ser Ser Gly Ala Ala Tyr Val
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tgc aaa gta gca gta gtc ggc gaa gcg act gtc ggc aag agc gcg ctc	96
Cys Lys Val Ala Val Val Gly Glu Ala Thr Val Gly Lys Ser Ala Leu	
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atc tct atg ttc acg agt aaa ggc agc aag ttt cta aag gac tat gcg	144
Ile Ser Met Phe Thr Ser Lys Gly Ser Lys Phe Leu Lys Asp Tyr Ala	
35 40 45	
atg acg agt ggg gtg gag gtg gtg gta gcc ccg gtg acc att ccg gac	192
Met Thr Ser Gly Val Glu Val Val Val Ala Pro Val Thr Ile Pro Asp	
50 55 60	
acg acg gtc tcg gtg gag ctc ttt ctg ctg gac acg gcg ggg agc gac	240
Thr Thr Val Ser Val Glu Leu Phe Leu Leu Asp Thr Ala Gly Ser Asp	
65 70 75 80	
ctg tac aag gag cag ata tcg cag tac tgg aac ggc gta tac tac gcc	288
Leu Tyr Lys Glu Gln Ile Ser Gln Tyr Trp Asn Gly Val Tyr Tyr Ala	
85 90 95	
att ctc gtg ttc gat gtg agc tct atg gag tcc ttc gag tcg tgc aag	336
Ile Leu Val Phe Asp Val Ser Ser Met Glu Ser Phe Glu Ser Cys Lys	
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gcg tgg ttt gag ctg ctc aaa tcg gcg cgt ccc gac cgc gag cgg ccg	384
Ala Trp Phe Glu Leu Leu Lys Ser Ala Arg Pro Asp Arg Glu Arg Pro	
115 120 125	
ctg cgc gcc gtg ctg gtg gcg aac aag acg gac ctt ccg ccg cag cgg	432
Leu Arg Ala Val Leu Val Ala Asn Lys Thr Asp Leu Pro Pro Gln Arg	
130 135 140	
cac cag gtg cgg ctg gac atg gcg cag gac tgg gcc acc acc aac acc	480
His Gln Val Arg Leu Asp Met Ala Gln Asp Trp Ala Thr Thr Asn Thr	
145 150 155 160	
ctc gac ttc ttc gac gtg tcc gcg aac ccg ccc ggc aag gac gcg gat	528
Leu Asp Phe Phe Asp Val Ser Ala Asn Pro Pro Gly Lys Asp Ala Asp	
165 170 175	
gcg ccg ttc ctg tcc atc gcc acc acc ttc tac cgc aac tac gag gac	576
Ala Pro Phe Leu Ser Ile Ala Thr Thr Phe Tyr Arg Asn Tyr Glu Asp	
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Ile Ser Met Phe Thr Ser Lys Gly Ser Lys Phe Leu Lys Asp Tyr Ala
          35          40          45
Met Thr Ser Gly Val Glu Val Val Val Ala Pro Val Thr Ile Pro Asp
          50          55          60
Thr Thr Val Ser Val Glu Leu Phe Leu Leu Asp Thr Ala Gly Ser Asp
          65          70          75          80
Leu Tyr Lys Glu Gln Ile Ser Gln Tyr Trp Asn Gly Val Tyr Tyr Ala
          85          90          95
Ile Leu Val Phe Asp Val Ser Ser Met Glu Ser Phe Glu Ser Cys Lys
          100          105          110
Ala Trp Phe Glu Leu Leu Lys Ser Ala Arg Pro Asp Arg Glu Arg Pro
          115          120          125
Leu Arg Ala Val Leu Val Ala Asn Lys Thr Asp Leu Pro Pro Gln Arg
          130          135          140
His Gln Val Arg Leu Asp Met Ala Gln Asp Trp Ala Thr Thr Asn Thr
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Leu Asp Phe Phe Asp Val Ser Ala Asn Pro Pro Gly Lys Asp Ala Asp
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Ala Pro Phe Leu Ser Ile Ala Thr Thr Phe Tyr Arg Asn Tyr Glu Asp
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Lys Val Ala Ala Phe Gln Asp Ala Cys Arg Asn Tyr
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<222> (1)...(1032)

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cag ttc cag ggc acc gcg cgc tcg cag gtc gtg cag aac cag ccg cac      96
Gln Phe Gln Gly Thr Ala Arg Ser Gln Val Val Gln Asn Gln Pro His
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gac gag gag gtg aac ctg agt gag tcg gag agc ttc gcg gga gcg gat      144
Asp Glu Glu Val Asn Leu Ser Glu Ser Glu Ser Phe Ala Gly Ala Asp
          35          40          45

gag cct cca gct gcg cct aga gat gcg tcg ctc ata gag tca cac gac      192
Glu Pro Pro Ala Ala Pro Arg Asp Ala Ser Leu Ile Glu Ser His Asp
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tat gag gct gga aag cac gca cct ggc ggc atc gcc aac tcg gac gag	288
Tyr Glu Ala Gly Lys His Ala Pro Gly Gly Ile Ala Asn Ser Asp Glu	
85 90 95	
gca ccg ccg ggt gct tac aac gca cag gag tac aag cac ctg aac gtg	336
Ala Pro Pro Gly Ala Tyr Asn Ala Gln Glu Tyr Lys His Leu Asn Val	
100 105 110	
ggc gag gac gtg cgc gag ctg ttc tcc tac atc ggc cgc tac aag ccg	384
Gly Glu Asp Val Arg Glu Leu Phe Ser Tyr Ile Gly Arg Tyr Lys Pro	
115 120 125	
cag acg gtg gag ctg gac acg cgc atc aag ccc ttc atc cct gac tac	432
Gln Thr Val Glu Leu Asp Thr Arg Ile Lys Pro Phe Ile Pro Asp Tyr	
130 135 140	
atc ccc gcg gtg ggc ggc atc gac gag ttc atc aag gtg ccg cga ccc	480
Ile Pro Ala Val Gly Gly Ile Asp Glu Phe Ile Lys Val Pro Arg Pro	
145 150 155 160	
gac acc aag ccc gac tac ctg ggg ctc aag gtt ctg gac gag ccg gcc	528
Asp Thr Lys Pro Asp Tyr Leu Gly Leu Lys Val Leu Asp Glu Pro Ala	
165 170 175	
gcc aag cag tcg gac ccc acg gtg ctg acg ctg cag ctg cgg cag ctg	576
Ala Lys Gln Ser Asp Pro Thr Val Leu Thr Leu Gln Leu Arg Gln Leu	
180 185 190	
tcc aag gag gcg ccg ggc gcc aag gcc gac atg gtg ggg cgg ctg gag	624
Ser Lys Glu Ala Pro Gly Ala Lys Ala Asp Met Val Gly Arg Leu Glu	
195 200 205	
cac acc gac gag aac aag gcc aag aag atc cag cag tgg atc gcc tcc	672
His Thr Asp Glu Asn Lys Ala Lys Lys Ile Gln Gln Trp Ile Ala Ser	
210 215 220	
atc aac gac atc cac aag gcc aag ccg gcc gcc acc gtc aac tac agc	720
Ile Asn Asp Ile His Lys Ala Lys Pro Ala Ala Thr Val Asn Tyr Ser	
225 230 235 240	
aag cgc atg cca gag atc gag gcg ctg atg cag gag tgg ccg ccg gag	768
Lys Arg Met Pro Glu Ile Glu Ala Leu Met Gln Glu Trp Pro Pro Glu	
245 250 255	
gtg gag acc ttc ctc aag acc atg cac atg ccg tcc ggc gat gtg gag	816
Val Glu Thr Phe Leu Lys Thr Met His Met Pro Ser Gly Asp Val Glu	
260 265 270	
ctg gac atc aag acc tac gcc cgg ctg gtg tgc acg ctg ctg gac att	864
Leu Asp Ile Lys Thr Tyr Ala Arg Leu Val Cys Thr Leu Leu Asp Ile	
275 280 285	

ccc gtg tac gac gac ccc gtg gag agc ctg cac gtg ctg ttc aca ctg 912
 Pro Val Tyr Asp Asp Pro Val Glu Ser Leu His Val Leu Phe Thr Leu
 290 295 300

tac ctg gag ttc aag aac aac ccc atc ttc agg cag cac atg gag atg 960
 Tyr Leu Glu Phe Lys Asn Asn Pro Ile Phe Arg Gln His Met Glu Met
 305 310 315 320

gag aac aag ctg gac ggc atg tcg ggc ggc ggc ggc ggc atg atg ggc 1008
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<211> 344

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<213> Chlamydomonas reinhardtii

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 35 40 45
 Glu Pro Pro Ala Ala Pro Arg Asp Ala Ser Leu Ile Glu Ser His Asp
 50 55 60
 Met Asp Glu Gly Pro Ala Ala Pro Ala Arg Thr Leu Ser Pro Thr Gly
 65 70 75 80
 Tyr Glu Ala Gly Lys His Ala Pro Gly Gly Ile Ala Asn Ser Asp Glu
 85 90 95
 Ala Pro Pro Gly Ala Tyr Asn Ala Gln Glu Tyr Lys His Leu Asn Val
 100 105 110
 Gly Glu Asp Val Arg Glu Leu Phe Ser Tyr Ile Gly Arg Tyr Lys Pro
 115 120 125
 Gln Thr Val Glu Leu Asp Thr Arg Ile Lys Pro Phe Ile Pro Asp Tyr
 130 135 140
 Ile Pro Ala Val Gly Gly Ile Asp Glu Phe Ile Lys Val Pro Arg Pro
 145 150 155 160
 Asp Thr Lys Pro Asp Tyr Leu Gly Leu Lys Val Leu Asp Glu Pro Ala
 165 170 175
 Ala Lys Gln Ser Asp Pro Thr Val Leu Thr Leu Gln Leu Arg Gln Leu
 180 185 190
 Ser Lys Glu Ala Pro Gly Ala Lys Ala Asp Met Val Gly Arg Leu Glu
 195 200 205
 His Thr Asp Glu Asn Lys Ala Lys Lys Ile Gln Gln Trp Ile Ala Ser
 210 215 220
 Ile Asn Asp Ile His Lys Ala Lys Pro Ala Ala Thr Val Asn Tyr Ser
 225 230 235 240
 Lys Arg Met Pro Glu Ile Glu Ala Leu Met Gln Glu Trp Pro Pro Glu
 245 250 255
 Val Glu Thr Phe Leu Lys Thr Met His Met Pro Ser Gly Asp Val Glu
 260 265 270

Leu	Asp	Ile	Lys	Thr	Tyr	Ala	Arg	Leu	Val	Cys	Thr	Leu	Leu	Asp	Ile
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Pro	Val	Tyr	Asp	Asp	Pro	Val	Glu	Ser	Leu	His	Val	Leu	Phe	Thr	Leu
	290					295					300				
Tyr	Leu	Glu	Phe	Lys	Asn	Asn	Pro	Ile	Phe	Arg	Gln	His	Met	Glu	Met
305					310					315					320
Glu	Asn	Lys	Leu	Asp	Gly	Met	Ser	Gly	Gly	Gly	Gly	Gly	Met	Met	Gly
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<220>

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gag	gtt	cgg	att	ctc	ttc	agc	aca	gcg	aag	ggg	gaa	tcc	cat	acg	cac			160
Glu	Val	Arg	Ile	Leu	Phe	Ser	Thr	Ala	Lys	Gly	Glu	Ser	His	Thr	His			
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aag	gca	ggc	ttc	aag	cag	cta	ttt	cga	cga	ttg	cgt	tca	act	tat	cgt			208
Lys	Ala	Gly	Phe	Lys	Gln	Leu	Phe	Arg	Arg	Leu	Arg	Ser	Thr	Tyr	Arg			
		25					30				35							
cca	gac	aaa	gta	gat	aag	gat	gac	ttc	acg	ctg	gac	acg	ctg	cgg	tca			256
Pro	Asp	Lys	Val	Asp	Lys	Asp	Asp	Phe	Thr	Leu	Asp	Thr	Leu	Arg	Ser			
	40					45					50				55			
gcg	cac	atc	ctt	gtg	ctc	ggt	ggc	ccg	aag	gag	aag	ttc	acc	gcg	cct			304
Ala	His	Ile	Leu	Val	Leu	Gly	Gly	Pro	Lys	Glu	Lys	Phe	Thr	Ala	Pro			
				60					65					70				
gag	gtg	gac	atg	ctc	aaa	aag	ttc	gtg	aag	aat	ggt	ggc	tcc	atc	ctc			352
Glu	Val	Asp	Met	Leu	Lys	Lys	Phe	Val	Lys	Asn	Gly	Gly	Ser	Ile	Leu			
			75						80					85				
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Ile	Leu	Met	Ser	Glu	Gly	Gly	Glu	Glu	Lys	Ala	Gly	Thr	Asn	Ile	Asn			
			90					95					100					
tac	ttc	ctc	gag	cag	ttt	ggc	atg	tcg	gtg	aac	aac	gac	gcc	gtg	gtc			448
Tyr	Phe	Leu	Glu	Gln	Phe	Gly	Met	Ser	Val	Asn	Asn	Asp	Ala	Val	Val			
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Arg	Thr	Thr	His	Tyr	Lys	Tyr	Leu	His	Pro	Lys	Glu	Val	Leu	Ile	Ser			
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 Leu Glu Leu Phe Asp Leu Asp Glu Ser Phe Ala Ser Glu Thr Asn Arg
 360 365 370 375

ctg gcc tcg ctc acc aac aag tgc cac ggc gag gag gac ctg gag tac 1264
 Leu Ala Ser Leu Thr Asn Lys Cys His Gly Glu Glu Asp Leu Glu Tyr
 380 385 390

tac atc atg gag gcg ggc cac atc ctg ggc ctc aag ctg cag gag aac 1312
 Tyr Ile Met Glu Ala Gly His Ile Leu Gly Leu Lys Leu Gln Glu Asn
 395 400 405

gcc aac gcc aag cac gtg ctg tcg gag gtg ttc cgc cgc atc gcg cag 1360
 Ala Asn Ala Lys His Val Leu Ser Glu Val Phe Arg Arg Ile Ala Gln
 410 415 420

tac aag atg ggc agc ctg ggc ctg ggc cag acg ctg gac tcc atg ggc 1408
 Tyr Lys Met Gly Ser Leu Gly Leu Gly Gln Thr Leu Asp Ser Met Gly
 425 430 435

cag acc ctg ccc gcg gcc aac cag ttc ggc gac cag ttc gag ctg 1453
 Gln Thr Leu Pro Ala Ala Asn Gln Phe Gly Asp Gln Phe Glu Leu
 440 445 450

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 35 40 45
 Thr Leu Asp Thr Leu Arg Ser Ala His Ile Leu Val Leu Gly Gly Pro
 50 55 60

Lys Glu Lys Phe Thr Ala Pro Glu Val Asp Met Leu Lys Lys Phe Val
 65 70 75 80
 Lys Asn Gly Gly Ser Ile Leu Ile Leu Met Ser Glu Gly Gly Glu Glu
 85 90 95
 Lys Ala Gly Thr Asn Ile Asn Tyr Phe Leu Glu Gln Phe Gly Met Ser
 100 105 110
 Val Asn Asn Asp Ala Val Val Arg Thr Thr His Tyr Lys Tyr Leu His
 115 120 125
 Pro Lys Glu Val Leu Ile Ser Asp Gly Ile Leu Asn Arg Ala Val Ile
 130 135 140
 Thr Gly Ala Gly Lys Ser Leu Asn Ser Asn Asp Asp Glu Phe Arg
 145 150 155 160
 Val Ser Arg Gly Pro Gln Ala Phe Asp Gly Thr Gly Leu Glu Tyr Val
 165 170 175
 Phe Pro Phe Gly Ala Thr Leu Ser Val Gln Lys Pro Ala Val Pro Val
 180 185 190
 Leu Ser Ser Gly Lys Ile Ala Tyr Pro Met Asn Arg Pro Val Gly Ala
 195 200 205
 Val Trp Ala Gln Pro Gly Tyr Gly Arg Ile Ala Val Leu Gly Ser Cys
 210 215 220
 Ala Met Phe Asp Asp Lys Trp Leu Asp Lys Glu Glu Asn Ser Lys Ile
 225 230 235 240
 Met Asp Phe Phe Phe Lys Phe Leu Glu Pro His Ser Lys Ile Gln Leu
 245 250 255
 Asn Asp Ile Asp Ala Glu Glu Pro Asp Val Ser Asp Leu Lys Leu Leu
 260 265 270
 Pro Asp Thr Ala Ser Leu Ala Asp Lys Leu Lys Gly Cys Leu Gln Glu
 275 280 285
 Ile Asp Asp Val Pro Arg Asp Trp Thr Ser Leu Phe Asp Asp Ser Leu
 290 295 300
 Phe Lys Phe Asp Thr Gly Leu Ile Pro Glu Ala Val Ser Leu Tyr Glu
 305 310 315 320
 Lys Leu Gly Val Lys Lys Gly Gln Leu Asn Leu Ile Pro Pro Ser Phe
 325 330 335
 Glu Thr Pro Leu Pro Pro Leu Gln Pro Ala Val Phe Pro Pro Thr Ile
 340 345 350
 Arg Glu Pro Pro Pro Pro Ala Leu Glu Leu Phe Asp Leu Asp Glu Ser
 355 360 365

 Phe Ala Ser Glu Thr Asn Arg Leu Ala Ser Leu Thr Asn Lys Cys His
 370 375 380
 Gly Glu Glu Asp Leu Glu Tyr Tyr Ile Met Glu Ala Gly His Ile Leu
 385 390 395 400
 Gly Leu Lys Leu Gln Glu Asn Ala Asn Ala Lys His Val Leu Ser Glu
 405 410 415
 Val Phe Arg Arg Ile Ala Gln Tyr Lys Met Gly Ser Leu Gly Leu Gly
 420 425 430
 Gln Thr Leu Asp Ser Met Gly Gln Thr Leu Pro Ala Ala Asn Gln Phe
 435 440 445
 Gly Asp Gln Phe Glu Leu
 450

<210> 9

<211> 1902

<212> DNA

<213> Chlamydomonas reinhardtii

<220>

<221> CDS

<222> (86)...(1492)

<400> 9

gtcttgaggaa cccagcgcgc gcgcctcctt gccacatgtc ctgctagctt ctgggtttaca	60
ccgtagattc atttaagcga gagac atg agc agc aag cgg ggt ggg cgg tca	112
Met Ser Ser Lys Arg Gly Gly Arg Ser	
1 5	
tcc tta gca aag gcg ccc gaa gag gcg gta aat ggc gag gca ttt gcg	160
Ser Leu Ala Lys Ala Pro Glu Glu Ala Val Asn Gly Glu Ala Phe Ala	
10 15 20 25	
cct gag gca tct ccc cct cca ccc ggc gac gat gga gat gct ggt ggg	208
Pro Glu Ala Ser Pro Pro Pro Gly Asp Asp Gly Asp Ala Gly Gly	
30 35 40	
gag gac ggt ggc gcg cct gcg ccc cct ccg ccc ccg gct aca aag ggc	256
Glu Asp Gly Gly Ala Pro Ala Pro Pro Pro Pro Ala Thr Lys Gly	
45 50 55	
ggt cca gta gct gta gga agg tcg ctg gag ata caa aca acg ccg gac	304
Gly Pro Val Ala Val Gly Arg Ser Leu Glu Ile Gln Thr Thr Pro Asp	
60 65 70	
gtg tgc atg gaa atg ctg gcc gac aag ctg aag ctg cta aac tac gag	352
Val Cys Met Glu Met Leu Ala Asp Lys Leu Lys Leu Leu Asn Tyr Glu	
75 80 85	
gcg gat ttc tgc agg aag aag aag ccc tac ccg aaa ccc ctc tcg ccg	400
Ala Asp Phe Cys Arg Lys Lys Lys Pro Tyr Arg Lys Pro Leu Ser Arg	
90 95 100 105	
ctc tat ttt gcg gtg ccg ctc gca aac tcg agc gag cag ttc ttc tac	448
Leu Tyr Phe Ala Val Pro Leu Ala Asn Ser Ser Glu Gln Phe Phe Tyr	
110 115 120	
ttt acc agt ctg gcg acc tgg ctg ctg ggc ctg gct ggc gtg gag ctg	496
Phe Thr Ser Leu Ala Thr Trp Leu Leu Gly Leu Ala Gly Val Glu Leu	
125 130 135	
ccc gct ccc aag gag ttt gat gac ccg aac ttg acg tgc cag aac atc	544
Pro Ala Pro Lys Glu Phe Asp Asp Pro Asn Leu Thr Cys Gln Asn Ile	
140 145 150	
ctg ggt gcg gtg aag aag ctg ggc ttt gcg ccg ccc agc tac cac cct	592
Leu Gly Ala Val Lys Lys Leu Gly Phe Ala Pro Pro Ser Tyr His Pro	
155 160 165	
acc aag ctc aca gtg ggc aac ggc aag gag gtg gtg ggt gtg ctg gac	640
Thr Lys Leu Thr Val Gly Asn Gly Lys Glu Val Val Gly Val Leu Asp	
170 175 180 185	

ggg ctg gtg gac ttc gtg ctg gag cgg cgg cac cac aag tac agc cgg Gly Leu Val Asp Phe Val Leu Glu Arg Arg His His Lys Tyr Ser Arg 190 195 200	688
ccc gcg tac gga aat gat ggg caa ccg gag gag ggc gtg caa ctg gac Pro Ala Tyr Gly Asn Asp Gly Gln Pro Glu Glu Gly Val Gln Leu Asp 205 210 215	736
gat gag gcg gag gct gcc gcg atg gag ggt gcg gat gag ctg gcg atg Asp Glu Ala Glu Ala Ala Ala Met Glu Gly Ala Asp Glu Leu Ala Met 220 225 230	784
cca gcc cag aac cag gcg gat gac gat gag gag gag gag ggc gta tac Pro Ala Gln Asn Gln Ala Asp Asp Asp Glu Glu Glu Glu Gly Val Tyr 235 240 245	832
gtg gac ccg ggg cgc ggt gac gcc gcg ggc cca ggg aca ggg gca tcc Val Asp Pro Gly Arg Gly Asp Ala Ala Gly Pro Gly Thr Gly Ala Ser 250 255 260 265	880
gcg gcg atg gac gcg gag aag gcg gtg ctt gtg tcc aag gtg gac ccc Ala Ala Met Asp Ala Glu Lys Ala Val Leu Val Ser Lys Val Asp Pro 270 275 280	928
acg ctc tgg aag atc gag ctg gag cgc gtg gcg ccg aag ctg cgt atc Thr Leu Trp Lys Ile Glu Leu Glu Arg Val Ala Pro Lys Leu Arg Ile 285 290 295	976
acc atc gcc gcc gac tcg aag gac tgg cgc tca cat ctg gat gag gcg Thr Ile Ala Ala Asp Ser Lys Asp Trp Arg Ser His Leu Asp Glu Ala 300 305 310	1024
cac cag cac aag gag gtg atc agc aag gcc tgg ccc gac agc aag acg His Gln His Lys Glu Val Ile Ser Lys Ala Trp Pro Asp Ser Lys Thr 315 320 325	1072
tcg ctg gag cgc ctg cgt gcg gac ctg aac ggc acg ctg gag aag ctg Ser Leu Glu Arg Leu Arg Ala Asp Leu Asn Gly Thr Leu Glu Lys Leu 330 335 340 345	1120
cag acg cgt gag aag ttc ctc aac gag cag ttt gag agc ctc atg cag Gln Thr Arg Glu Lys Phe Leu Asn Glu Gln Phe Glu Ser Leu Met Gln 350 355 360	1168
cag tac cgc gcc gcc cgc acc acg ttc acg gac gtg cag gag aca tac Gln Tyr Arg Ala Ala Arg Thr Thr Phe Thr Asp Val Gln Glu Thr Tyr 365 370 375	1216
aac cgc aag acg gag gcg gtg gcg gac cgg aac cag gag atg cac cgc Asn Arg Lys Thr Glu Ala Val Ala Asp Arg Asn Gln Glu Met His Arg 380 385 390	1264
atc ggc gag acg ctg gag gag gtg aag gcc atg atg gac gag aag ggc Ile Gly Glu Thr Leu Glu Glu Val Lys Ala Met Met Asp Glu Lys Gly 395 400 405	1312

agc aac atc gcg gac gcc acg cct gtg gct cgc atc aag acc gcc atc 1360
 Ser Asn Ile Ala Asp Ala Thr Pro Val Ala Arg Ile Lys Thr Ala Ile
 410 415 420 425

aag cag ctt aac aag gag ctg cac gac atg gag gtg cgc atc ggc gtg 1408
 Lys Gln Leu Asn Lys Glu Leu His Asp Met Glu Val Arg Ile Gly Val
 430 435 440

gtt agc cac acg ctg ctg cag cta tcg ctg cgc aac aag cga ttg ctg 1456
 Val Ser His Thr Leu Leu Gln Leu Ser Leu Arg Asn Lys Arg Leu Leu
 445 450 455

cag gcg cag gcg gct ctc agt gac gag gag gag gac tagctagatc 1502
 Gln Ala Gln Ala Ala Leu Ser Asp Glu Glu Glu Asp
 460 465

agcgaagtgc agagggcatg tgtgcgtacc gtgtgcgcgg gtacagccgt gggatggaag 1562
 aggtgatgtg gcgggttgcg gaccagcat tcggtagacc agatcactta taggtacaga 1622
 aagacggcta tattgttggg ggccggcgac cctggctatg tatatacaag ccgtagcgca 1682
 gagccgctgc aaatgcggtg ctgtgcctgt gctcccgtgg gtgtgcgcgg ttccggtcaa 1742
 gttcatataa gctgttgta cttgtgaggc aggcattggca tatggacagg gcatccctgc 1802
 aaggaaagca ggcagcggtg tccttgtggc gatgggtcaa gcagtgatgg aggggcgaag 1862
 cgagttgcgg gcctgtaagc acaggggtgc caaaaaaaaaa 1902

<210> 10

<211> 469

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 10

Met Ser Ser Lys Arg Gly Gly Arg Ser Ser Leu Ala Lys Ala Pro Glu
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 Glu Ala Val Asn Gly Glu Ala Phe Ala Pro Glu Ala Ser Pro Pro Pro
 20 25 30
 Pro Gly Asp Asp Gly Asp Ala Gly Gly Glu Asp Gly Gly Ala Pro Ala
 35 40 45
 Pro Pro Pro Pro Pro Ala Thr Lys Gly Gly Pro Val Ala Val Gly Arg
 50 55 60
 Ser Leu Glu Ile Gln Thr Thr Pro Asp Val Cys Met Glu Met Leu Ala
 65 70 75 80
 Asp Lys Leu Lys Leu Leu Asn Tyr Glu Ala Asp Phe Cys Arg Lys Lys
 85 90 95
 Lys Pro Tyr Arg Lys Pro Leu Ser Arg Leu Tyr Phe Ala Val Pro Leu
 100 105 110
 Ala Asn Ser Ser Glu Gln Phe Phe Tyr Phe Thr Ser Leu Ala Thr Trp
 115 120 125
 Leu Leu Gly Leu Ala Gly Val Glu Leu Pro Ala Pro Lys Glu Phe Asp
 130 135 140
 Asp Pro Asn Leu Thr Cys Gln Asn Ile Leu Gly Ala Val Lys Lys Leu
 145 150 155 160
 Gly Phe Ala Pro Pro Ser Tyr His Pro Thr Lys Leu Thr Val Gly Asn
 165 170 175
 Gly Lys Glu Val Val Gly Val Leu Asp Gly Leu Val Asp Phe Val Leu
 180 185 190
 Glu Arg Arg His His Lys Tyr Ser Arg Pro Ala Tyr Gly Asn Asp Gly
 195 200 205

Gln Pro Glu Glu Gly Val Gln Leu Asp Asp Glu Ala Glu Ala Ala Ala
 210 215 220
 Met Glu Gly Ala Asp Glu Leu Ala Met Pro Ala Gln Asn Gln Ala Asp
 225 230 235 240
 Asp Asp Glu Glu Glu Glu Gly Val Tyr Val Asp Pro Gly Arg Gly Asp
 245 250 255
 Ala Ala Gly Pro Gly Thr Gly Ala Ser Ala Ala Met Asp Ala Glu Lys
 260 265 270
 Ala Val Leu Val Ser Lys Val Asp Pro Thr Leu Trp Lys Ile Glu Leu
 275 280 285
 Glu Arg Val Ala Pro Lys Leu Arg Ile Thr Ile Ala Ala Asp Ser Lys
 290 295 300
 Asp Trp Arg Ser His Leu Asp Glu Ala His Gln His Lys Glu Val Ile
 305 310 315 320
 Ser Lys Ala Trp Pro Asp Ser Lys Thr Ser Leu Glu Arg Leu Arg Ala
 325 330 335
 Asp Leu Asn Gly Thr Leu Glu Lys Leu Gln Thr Arg Glu Lys Phe Leu
 340 345 350
 Asn Glu Gln Phe Glu Ser Leu Met Gln Gln Tyr Arg Ala Ala Arg Thr
 355 360 365
 Thr Phe Thr Asp Val Gln Glu Thr Tyr Asn Arg Lys Thr Glu Ala Val
 370 375 380
 Ala Asp Arg Asn Gln Glu Met His Arg Ile Gly Glu Thr Leu Glu Glu
 385 390 395 400
 Val Lys Ala Met Met Asp Glu Lys Gly Ser Asn Ile Ala Asp Ala Thr
 405 410 415
 Pro Val Ala Arg Ile Lys Thr Ala Ile Lys Gln Leu Asn Lys Glu Leu
 420 425 430
 His Asp Met Glu Val Arg Ile Gly Val Val Ser His Thr Leu Leu Gln
 435 440 445
 Leu Ser Leu Arg Asn Lys Arg Leu Leu Gln Ala Gln Ala Ala Leu Ser
 450 455 460
 Asp Glu Glu Glu Asp
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 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (59)...(1345)

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 atg gcc gcc gcg gcc gcg gtg atc ccg ccg tcg ggc ttg gac gat ggg 106
 Met Ala Ala Ala Ala Ala Val Ile Pro Pro Ser Gly Leu Asp Asp Gly
 1 5 10 15
 gtg tct cgg gct cgc ggg gaa ggc gca ggg gag gct gtg gtg gag cgc 154
 Val Ser Arg Ala Arg Gly Glu Gly Ala Gly Glu Ala Val Val Glu Arg
 20 25 30
 ggg cca gga gcg gcc tac cac atg ttc gtg gtg atg gaa gac tta gtg 202
 Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
 35 40 45

gag aag ctg aag ctg ctc cgc tac gag gag gag cta ctc cga aag agc Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Glu Leu Leu Arg Lys Ser 50 55 60	250
aat ctg aag ccc ccg tcc aga cac tac ttt gct ctg cct acc aac cca Asn Leu Lys Pro Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro 65 70 75 80	298
ggc gag cag ttc tac atg ttt tgc act ctt gct gcg tgg ctg atc aac Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn 85 90 95	346
aaa act ggc cgt gcc ttt gag cag cct caa gaa tac gac gat ccc aat Lys Thr Gly Arg Ala Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn 100 105 110	394
gca act ata tct aat ata ctc tct gag ctt cgc tct ttt ggg aga act Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr 115 120 125	442
gca gat ttt cct cct tca aaa tta aag tct ggt tac gga gaa caa gtg Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu Gln Val 130 135 140	490
tgc tat gtt ctt gat tgc tta gct gaa gaa gct tta aaa tat att ggt Cys Tyr Val Leu Asp Cys Leu Ala Glu Glu Ala Leu Lys Tyr Ile Gly 145 150 155 160	538
ttc act tgg aaa agg cca tca tac cca gtg gaa gaa cta gaa gaa gaa Phe Thr Trp Lys Arg Pro Ser Tyr Pro Val Glu Glu Leu Glu Glu Glu 165 170 175	586
act gtt cca gaa gat gat gcc gag tta aca tta agt aaa gtg gat gaa Thr Val Pro Glu Asp Asp Ala Glu Leu Thr Leu Ser Lys Val Asp Glu 180 185 190	634
gaa ttt gtg gaa gag gag aca gat aat gaa gaa aac ttt att gat ctc Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu 195 200 205	682
aac gtt tta aag gcc cag acc tat cgc ttg gac aca aac gag tct gcc Asn Val Leu Lys Ala Gln Thr Tyr Arg Leu Asp Thr Asn Glu Ser Ala 210 215 220	730
aaa caa gaa gat att ttg gaa tct acg aca gat gct gcg gaa tgg agc Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser 225 230 235 240	778
cta gaa gtt gag cgt gta cta ccg cag ctg aaa gtc acg att agg act Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr 245 250 255	826
gac aat aag gat tgg agg atc cat gtt gac caa atg cac cag cac aaa Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Lys 260 265 270	874

922

970

1018

1066

1114

1162

1210

1258

1306

1355

1415

1475

1535

1559

Glu	Lys	Leu	Lys	Leu	Leu	Arg	Tyr	Glu	Glu	Glu	Leu	Leu	Arg	Lys	Ser	50	55	60
Asn	Leu	Lys	Pro	Pro	Ser	Arg	His	Tyr	Phe	Ala	Leu	Pro	Thr	Asn	Pro	65	70	75
Gly	Glu	Gln	Phe	Tyr	Met	Phe	Cys	Thr	Leu	Ala	Ala	Trp	Leu	Ile	Asn	85	90	95
Lys	Thr	Gly	Arg	Ala	Phe	Glu	Gln	Pro	Gln	Glu	Tyr	Asp	Asp	Pro	Asn	100	105	110
Ala	Thr	Ile	Ser	Asn	Ile	Leu	Ser	Glu	Leu	Arg	Ser	Phe	Gly	Arg	Thr	115	120	125
Ala	Asp	Phe	Pro	Pro	Ser	Lys	Leu	Lys	Ser	Gly	Tyr	Gly	Glu	Gln	Val	130	135	140
Cys	Tyr	Val	Leu	Asp	Cys	Leu	Ala	Glu	Glu	Ala	Leu	Lys	Tyr	Ile	Gly	145	150	155
Phe	Thr	Trp	Lys	Arg	Pro	Ser	Tyr	Pro	Val	Glu	Glu	Leu	Glu	Glu	Glu	165	170	175
Thr	Val	Pro	Glu	Asp	Asp	Ala	Glu	Leu	Thr	Leu	Ser	Lys	Val	Asp	Glu	180	185	190
Glu	Phe	Val	Glu	Glu	Glu	Thr	Asp	Asn	Glu	Glu	Asn	Phe	Ile	Asp	Leu	195	200	205
Asn	Val	Leu	Lys	Ala	Gln	Thr	Tyr	Arg	Leu	Asp	Thr	Asn	Glu	Ser	Ala	210	215	220
Lys	Gln	Glu	Asp	Ile	Leu	Glu	Ser	Thr	Thr	Asp	Ala	Ala	Glu	Trp	Ser	225	230	235
Leu	Glu	Val	Glu	Arg	Val	Leu	Pro	Gln	Leu	Lys	Val	Thr	Ile	Arg	Thr	245	250	255
Asp	Asn	Lys	Asp	Trp	Arg	Ile	His	Val	Asp	Gln	Met	His	Gln	His	Lys	260	265	270
Ser	Gly	Ile	Glu	Ser	Ala	Leu	Lys	Glu	Thr	Lys	Gly	Phe	Leu	Asp	Lys	275	280	285
Leu	His	Asn	Glu	Ile	Ser	Arg	Thr	Leu	Glu	Lys	Ile	Gly	Ser	Arg	Glu	290	295	300
Lys	Tyr	Ile	Asn	Asn	Gln	Leu	Glu	His	Leu	Val	Gln	Glu	Tyr	Arg	Gly	305	310	315
Ala	Gln	Ala	Gln	Leu	Ser	Glu	Ala	Arg	Glu	Arg	Tyr	Gln	Gln	Gly	Asn	325	330	335
Gly	Gly	Val	Thr	Glu	Arg	Thr	Arg	Leu	Leu	Ser	Glu	Val	Thr	Glu	Glu	340	345	350
Leu	Glu	Lys	Val	Lys	Gln	Glu	Met	Glu	Glu	Lys	Gly	Ser	Ser	Met	Thr	355	360	365
Asp	Gly	Thr	Pro	Leu	Val	Lys	Ile	Lys	Gln	Ser	Leu	Thr	Lys	Leu	Lys	370	375	380
Gln	Glu	Thr	Val	Gln	Met	Asp	Ile	Arg	Ile	Gly	Val	Val	Glu	His	Thr	385	390	395
Leu	Leu	Gln	Ser	Lys	Leu	Lys	Glu	Lys	Cys	Asn	Met	Thr	Arg	Asp	Met	405	410	415
His	Ala	Ala	Val	Thr	Pro	Glu	Ser	Ala	Ile	Gly	Phe	Tyr				420	425	

<210> 13

<211> 1954

<212> DNA

<213> Chlamydomonas reinhardtii

<220>

<221> CDS

<222> (1)...(1302)

<400> 13

gtg	tac	gtg	atc	cag	cag	gag	ttc	gcg	gcg	ctc	aag	gac	cgc	aac	gag	48
Val	Tyr	Val	Ile	Gln	Gln	Glu	Phe	Ala	Ala	Leu	Lys	Asp	Arg	Asn	Glu	
1				5				10						15		

cag	cag	cg	aag	cg	gtg	gac	gag	gtg	ctc	acg	gag	cg	ctc	aac	ctc	96
Gln	Gln	Arg	Lys	Arg	Val	Asp	Glu	Val	Leu	Thr	Glu	Arg	Leu	Asn	Leu	
			20				25						30			

gag	tcc	aag	gcc	aag	cag	gcc	gag	tcc	aag	atg	tct	gag	atc	cag	gag	144
Glu	Ser	Lys	Ala	Lys	Gln	Ala	Glu	Ser	Lys	Met	Ser	Glu	Ile	Gln	Ala	
		35					40					45				

tcc	atg	gac	cag	cg	ctc	aac	tct	atg	ccg	ccc	agc	cag	cg	aac	gaa	192
Ser	Met	Asp	Gln	Arg	Leu	Asn	Ser	Met	Pro	Pro	Ser	Gln	Arg	Asn	Glu	
	50					55					60					

tac	acc	acg	ctc	gtg	gcc	gag	cag	cag	cag	ctg	cag	gcc	gac	agc	aag	240
Tyr	Thr	Thr	Leu	Val	Ala	Glu	Gln	Gln	Gln	Leu	Gln	Ala	Asp	Ser	Lys	
65				70						75					80	

cg	ttt	gag	gag	gtg	ctg	gac	gag	ctg	gac	aag	gcg	ctg	cag	gcc	agc	288
Arg	Phe	Glu	Glu	Val	Leu	Asp	Glu	Leu	Asp	Lys	Ala	Leu	Gln	Ala	Ser	
				85					90					95		

gag	ggc	gag	ctg	gcg	cg	aac	ccc	ttc	aag	cag	cg	agc	ctg	cag	ctg	336
Glu	Gly	Glu	Leu	Ala	Arg	Asn	Pro	Phe	Lys	Gln	Arg	Ser	Leu	Gln	Leu	
			100					105					110			

cag	gag	cag	atc	cg	gcg	ctc	acg	ggg	aag	aag	tac	gag	ctg	acg	gag	384
Gln	Glu	Gln	Ile	Arg	Ala	Leu	Thr	Gly	Lys	Lys	Tyr	Glu	Leu	Thr	Glu	
			115				120						125			

gag	gag	cg	cag	agc	aag	cg	tcg	ccc	gag	gag	ctg	cg	gcc	gac	ctc	432
Glu	Glu	Arg	Gln	Ser	Lys	Arg	Ser	Pro	Glu	Glu	Leu	Arg	Ala	Asp	Leu	
		130				135					140					

atg	gcc	aag	atc	aag	cga	gac	aac	acc	gag	gtg	gag	cag	atg	acg	cag	480
Met	Ala	Lys	Ile	Lys	Arg	Asp	Asn	Thr	Glu	Val	Glu	Gln	Met	Thr	Gln	
145					150					155					160	

cag	atc	cg	gag	ctt	cag	gac	cag	atc	aag	aag	atg	gag	gag	cg	gtc	528
Gln	Ile	Arg	Glu	Leu	Gln	Asp	Gln	Ile	Lys	Lys	Met	Glu	Glu	Arg	Val	
			165						170					175		

aag	agc	ctg	ggc	ggc	gcc	acc	agc	ggc	gcg	gtg	gcg	gcg	gag	gaa	aag	576
Lys	Ser	Leu	Gly	Gly	Ala	Thr	Ser	Gly	Ala	Val	Ala	Ala	Glu	Glu	Lys	
			180					185					190			

gcc	aac	cg	gag	aag	ttt	gag	gag	ctg	ttg	gcc	aag	gag	cg	cac	cta	624
Ala	Asn	Arg	Glu	Lys	Phe	Glu	Glu	Leu	Leu	Ala	Lys	Glu	Arg	His	Leu	
		195				200						205				

aac	aac	ttt	atg	gac	ggc	ttc	ccc	agc	cg	aag	gcc	gcc	aag	atg	cag	672
Asn	Asn	Phe	Met	Asp	Gly	Phe	Pro	Ser	Arg	Lys	Ala	Ala	Lys	Met	Gln	
		210				215					220					

gag aag cag cag aag gag gac ggc atc gtg ggc gtg ctg gag aag atg Glu Lys Gln Gln Lys Glu Asp Gly Ile Val Gly Val Leu Glu Lys Met 225 230 235 240	720
gtg aag atg cag ggc atc att ggc tcc aac ctg ccc agc cag aag aag Val Lys Met Gln Gly Ile Ile Gly Ser Asn Leu Pro Ser Gln Lys Lys 245 250 255	768
tac aag gaa atg cag gac gag ctc gag tac aag aag atg cag ctg gag Tyr Lys Glu Met Gln Asp Glu Leu Glu Tyr Lys Lys Met Gln Leu Glu 260 265 270	816
aac acg cag acc acg cag gag cgg ctc aag gag gag ctg acc atg cgg Asn Thr Gln Thr Thr Gln Glu Arg Leu Lys Glu Glu Leu Thr Met Arg 275 280 285	864
cgc aca gag ctg gag aag atc gat acg ctg gag gac aag atc aag ctg Arg Thr Glu Leu Glu Lys Ile Asp Thr Leu Glu Asp Lys Ile Lys Leu 290 295 300	912
gag ctg acg cag ctg gcg gag cgg cag gag gcc atg gag aag gag atg Glu Leu Thr Gln Leu Ala Glu Arg Gln Glu Ala Met Glu Lys Glu Met 305 310 315 320	960
ggc gag ttc ggc agc gtc gag gac atc cag cgc aag gcc aac gcc gca Gly Glu Phe Gly Ser Val Glu Asp Ile Gln Arg Lys Ala Asn Ala Ala 325 330 335	1008
cgc gag cgc atg ggg gcc tgc gca gtg tgc tgt ttg aag cgc aag gac Arg Glu Arg Met Gly Ala Cys Ala Val Cys Cys Leu Lys Arg Lys Asp 340 345 350	1056
ctg ctg cgc tcc atc gtg gcg gag cgc ggc ctc aag ttc cag gcc aag Leu Leu Arg Ser Ile Val Ala Glu Arg Gly Leu Lys Phe Gln Ala Lys 355 360 365	1104
cgc gcg cag ctg cag gac cac aac ctc cag gtg cag ctg gag aag atg Arg Ala Gln Leu Gln Asp His Asn Leu Gln Val Gln Leu Glu Lys Met 370 375 380	1152
gag gcc aag ctg aag aat ctg agc gcg ggc gta ttc gag atg gac gag Glu Ala Lys Leu Lys Asn Leu Ser Ala Gly Val Phe Glu Met Asp Glu 385 390 395 400	1200
ttc atc aag gcc aag gag agc gag acc aac tac cgc cag ctg gcc tcc Phe Ile Lys Ala Lys Glu Ser Glu Thr Asn Tyr Arg Gln Leu Ala Ser 405 410 415	1248
aac ata gcg gcg ctg gta gac gac ctc aac gtg cat gtc aag aag gcc Asn Ile Ala Ala Leu Val Asp Asp Leu Asn Val His Val Lys Lys Ala 420 425 430	1296

gtg gtg taagaaggag gcagtgggtgt aaggggtctc cggaggaggg cgcgtgccgt 1352
Val Val

tggtgggggtg ttggggggcgc ggcgcgagaa gtacgtgcgt gtggcggtgt gcctttcagc 1412
aggctgcacg tgtagtacgg tagtcaaggt gaagggcggc ctggggcacag gaggatgctg 1472
acgccgtgac ggggtgacgat gacaggccat cgcgagttg atctctgctg tcgagtcatt 1532
gacttgggtt cctagacagg tcgggctaca agcccggagg ttgatggctc acctcgcagt 1592
gcgcggacag caggtgtggc gcatgcgcat gtgcctcagg agcgcggtgc ggaccaggga 1652
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gtacgatgtc agaagtggag ctaccgcccc tgcacaaggg gtgatgtaca tactgttatt 1832
taggagtcgg ctgcttatag ctactggact gcagaagaag gaggctgcaa ggatctgatg 1892
gaggcgctgg tgtgtatgga tgacgctgta agagatgcac aagagaaaaa aaaaaaaaaa 1952
aa 1954

<210> 14
<211> 434
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 14
Val Tyr Val Ile Gln Gln Glu Phe Ala Ala Leu Lys Asp Arg Asn Glu
1 5 10 15
Gln Gln Arg Lys Arg Val Asp Glu Val Leu Thr Glu Arg Leu Asn Leu
20 25 30
Glu Ser Lys Ala Lys Gln Ala Glu Ser Lys Met Ser Glu Ile Gln Ala
35 40 45
Ser Met Asp Gln Arg Leu Asn Ser Met Pro Pro Ser Gln Arg Asn Glu
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Tyr Thr Thr Leu Val Ala Glu Gln Gln Gln Leu Gln Ala Asp Ser Lys
65 70 75 80
Arg Phe Glu Glu Val Leu Asp Glu Leu Asp Lys Ala Leu Gln Ala Ser
85 90 95
Glu Gly Glu Leu Ala Arg Asn Pro Phe Lys Gln Arg Ser Leu Gln Leu
100 105 110
Gln Glu Gln Ile Arg Ala Leu Thr Gly Lys Lys Tyr Glu Leu Thr Glu
115 120 125
Glu Glu Arg Gln Ser Lys Arg Ser Pro Glu Glu Leu Arg Ala Asp Leu
130 135 140
Met Ala Lys Ile Lys Arg Asp Asn Thr Glu Val Glu Gln Met Thr Gln
145 150 155 160
Gln Ile Arg Glu Leu Gln Asp Gln Ile Lys Lys Met Glu Glu Arg Val
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Lys Ser Leu Gly Gly Ala Thr Ser Gly Ala Val Ala Ala Glu Glu Lys
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Ala Asn Arg Glu Lys Phe Glu Glu Leu Leu Ala Lys Glu Arg His Leu
195 200 205
Asn Asn Phe Met Asp Gly Phe Pro Ser Arg Lys Ala Ala Lys Met Gln
210 215 220
Glu Lys Gln Gln Lys Glu Asp Gly Ile Val Gly Val Leu Glu Lys Met
225 230 235 240
Val Lys Met Gln Gly Ile Ile Gly Ser Asn Leu Pro Ser Gln Lys Lys
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Tyr Lys Glu Met Gln Asp Glu Leu Glu Tyr Lys Lys Met Gln Leu Glu
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                               Met Ser Tyr
                               1

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g g g g g c a c g g a g g a g a t g a c c t t t a t g g a g g a t a t g a t g a g c a a t c g 164
Gly Gly Thr Glu Glu Asp Asp Leu Tyr Gly Gly Tyr Asp Glu Gln Ser
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aac ccg ctt gcg ggc tcg ggt ggt gcc gca ttt aag gca ctt ggg gcc 212
Asn Pro Leu Ala Gly Ser Gly Gly Ala Ala Phe Lys Ala Leu Gly Ala
20 25 30 35

gat gga gct cct cca ggc acc gcc atg atg ggg ccg cct ggc acg gcc 260
Asp Gly Ala Pro Pro Gly Thr Ala Met Met Gly Pro Pro Gly Thr Ala
40 45 50

atg aag agc ttc gtg cca ggc acg gct atg cgg ggc ggc acg gcg atg 308
Met Lys Ser Phe Val Pro Gly Thr Ala Met Arg Gly Gly Thr Ala Met
55 60 65

cag cag gac ccc agc ctg gcg cgg cct atg acc tcg aac cgg ggt gct 356
Gln Gln Asp Pro Ser Leu Ala Arg Pro Met Thr Ser Asn Arg Gly Ala
70 75 80

ggc ttc acg tcg gcg cct aac aag aag ttt gac ccc ctc aat cgc tca Gly Phe Thr Ser Ala Pro Asn Lys Lys Phe Asp Pro Leu Asn Arg Ser 85 90 95	404
atg ggg tcg aca ctg ggc tcg tcg ggg ggt ggc gca atg ctg gtg gct Met Gly Ser Thr Leu Gly Ser Ser Gly Gly Gly Ala Met Leu Val Ala 100 105 110 115	452
cgc aag ggt gac acc agc ccg gag gag cag gcg cgc ggg atg gag aag Arg Lys Gly Asp Thr Ser Pro Glu Glu Gln Ala Arg Gly Met Glu Lys 120 125 130	500
acg gtg cat gag ctg ctt gag aag agc gcg gcg gac gcg gct aag aat Thr Val His Glu Leu Leu Glu Lys Ser Ala Ala Asp Ala Ala Lys Asn 135 140 145	548
gac atc aac tcg gcc ctg gag aac gcc atg gag gcg aag aag aat gag Asp Ile Asn Ser Ala Leu Glu Asn Ala Met Glu Ala Lys Lys Asn Glu 150 155 160	596
cga aag ctg tgc cgc ttc cgg gaa cag aac aac atg gcg gac cag atc Arg Lys Leu Cys Arg Phe Arg Glu Gln Asn Asn Met Ala Asp Gln Ile 165 170 175	644
aac ctg gag ctg atg tac gcc gtg gac ttc aac ctg gca cac atg tac Asn Leu Glu Leu Met Tyr Ala Val Asp Phe Asn Leu Ala His Met Tyr 180 185 190 195	692
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cca tcc agc gag atg gat gac gat gac gac gac gac ccc atg ggc gat Pro Ser Ser Glu Met Asp Asp Asp Asp Asp Asp Pro Met Gly Asp 325 330 335	1124
gac gac atg caa gtg atg acc atg gat gac ggg ctg aag gac gag atg Asp Asp Met Gln Val Met Thr Met Asp Asp Gly Leu Lys Asp Glu Met 340 345 350 355	1172
cgc aag cgc aac acc atc atc acg cgc ctc att gtc aag gcc gcg cag Arg Lys Arg Asn Thr Ile Ile Thr Arg Leu Ile Val Lys Ala Ala Gln 360 365 370	1220
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ccc gcc gcg ctg ggc aag tac aag caa atc cac acg cag cac ccc gac Pro Ala Ala Leu Gly Lys Tyr Lys Gln Ile His Thr Gln His Pro Asp 660 665 670 675	2132
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ggc agc agc gcg gtg tcg gcg cag aac cgc ggc aag aag atg ctg gtc Gly Ser Ser Ala Val Ser Ala Gln Asn Arg Gly Lys Lys Met Leu Val 740 745 750 755	2372

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 Lys Glu His Met Gly Gly Gly Gly Gly Lys Asp Asn Asp Asp Trp Gly
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 Asn Glu Gln Leu Gly Asp Asp Leu Leu Pro Met
 775 780

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<213> Chlamydomonas reinhardtii

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 Gly Thr Ala Met Lys Ser Phe Val Pro Gly Thr Ala Met Arg Gly Gly
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 Thr Ala Met Gln Gln Asp Pro Ser Leu Ala Arg Pro Met Thr Ser Asn
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 Arg Gly Ala Gly Phe Thr Ser Ala Pro Asn Lys Lys Phe Asp Pro Leu
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 Asn Arg Ser Met Gly Ser Thr Leu Gly Ser Ser Gly Gly Gly Ala Met
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 Leu Val Ala Arg Lys Gly Asp Thr Ser Pro Glu Glu Gln Ala Arg Gly
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 Ala Lys Asn Asp Ile Asn Ser Ala Leu Glu Asn Ala Met Glu Ala Lys
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 Lys Asn Glu Arg Lys Leu Cys Arg Phe Arg Glu Gln Asn Asn Met Ala
 165 170 175
 Asp Gln Ile Asn Leu Glu Leu Met Tyr Ala Val Asp Phe Asn Leu Ala
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 His Met Tyr His Met Asn Lys Asn Tyr Ser Glu Ala Leu Asn Leu Tyr
 195 200 205

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Ile	Lys	Met	Tyr	Arg	Met	Ala	Leu	Asp	Gln	Ile	Ser	Ala	Thr	Ala	Lys
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Glu	Val	Arg	Phe	Lys	Ile	Met	Arg	Asn	Ile	Gly	Leu	Ser	Phe	Val	Arg
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Met	Gly	Gln	Tyr	Pro	Asp	Ala	Leu	Gln	Ser	Phe	Ala	Thr	Val	Met	Asp
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Asn	Val	Pro	Asp	His	Gln	Thr	Gly	Tyr	Asn	Leu	Val	Met	Cys	Asn	Tyr
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Lys	Val	Ser	Pro	Ser	Ser	Glu	Met	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Pro
				325					330					335	
Met	Gly	Asp	Asp	Asp	Met	Gln	Val	Met	Thr	Met	Asp	Asp	Gly	Leu	Lys
			340					345					350		
Asp	Glu	Met	Arg	Lys	Arg	Asn	Thr	Ile	Ile	Thr	Arg	Leu	Ile	Val	Lys
			355				360					365			
Ala	Ala	Gln	Leu	Ile	Ser	Glu	Lys	Val	Asp	Arg	Ala	Asn	Gly	Phe	Glu
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Lys	Leu	Ala	Asn	Glu	Val	Glu	Leu	Ala	Lys	Ala	Thr	Arg	Phe	Met	Gly
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Gln	Lys	Gln	Phe	Asp	Lys	Ala	Val	Gly	Val	Phe	Lys	Asp	Phe	Glu	Lys
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Lys	Glu	Pro	Arg	Val	Lys	Ala	Arg	Ala	Ala	Thr	Asn	Leu	Ala	Phe	Leu
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Tyr	Phe	Leu	Glu	Gly	Glu	Thr	Asp	Gln	Ala	Asp	Lys	Tyr	Ser	Glu	Met
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Ala	Leu	Lys	Ser	Asp	Arg	Tyr	Asn	Ala	Arg	Ala	Tyr	Val	Asn	Lys	Gly
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Cys	Val	Leu	Val	Glu	Arg	Gly	Asp	Leu	Glu	Gly	Ala	Arg	Ser	Leu	Phe
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Asn	Glu	Ala	Ala	Gly	Ile	Asp	Pro	Tyr	Cys	Val	Glu	Ala	Ile	Tyr	Asn
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Leu	Gly	Leu	Val	Ser	Gln	Arg	Leu	Asn	Glu	Leu	Pro	Tyr	Ala	Leu	Ala
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Ala	Phe	Lys	Lys	Leu	His	Asn	Met	Val	Pro	Asp	Asn	Val	Glu	Val	Ile
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His	Gln	Ile	Ala	Thr	Thr	Tyr	Asp	Met	Met	Gly	Asp	Phe	Lys	Asn	Ala
545					550					555					560
Val	Lys	Trp	Phe	Glu	Leu	Leu	Thr	Ser	Leu	Val	Ser	Asn	Asp	Pro	Gly
				565					570					575	
Val	Leu	Ala	Arg	Leu	Gly	Ala	Ile	His	Ala	Arg	Phe	Asp	Asp	Glu	Ala
			580					585				590			
Lys	Ala	Leu	His	Tyr	Tyr	Gln	Glu	Ser	His	Arg	Val	Tyr	Pro	Val	Asn
		595				600						605			
Met	Asp	Val	Ile	Ser	Trp	Leu	Gly	Ala	Tyr	His	Val	Lys	Ser	Glu	Val
610						615					620				
Tyr	Glu	Lys	Ala	Met	Pro	Phe	Phe	Asp	Leu	Ala	Ser	Lys	Ile	Gln	Pro
625					630					635					640
Gln	Glu	Val	Lys	Trp	Ala	Leu	Met	Val	Ala	Ser	Cys	Tyr	Arg	Arg	Thr
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Asn Asn Leu Pro Ala Ala Leu Gly Lys Tyr Lys Gln Ile His Thr Gln
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His Pro Asp Asn Val Glu Cys Leu Arg Tyr Leu Val His Leu Cys Ser
    675                      680                      685
Glu Leu Gly Arg Arg Ala Glu Ala Ala Glu Tyr Met Thr Lys Leu Lys
    690                      695                      700
Lys Ala Glu Lys Ala Ala Val Pro Glu Ala Thr Thr Ala Ala Ala Pro
    705                      710                      715                      720
Ala Ala Ala Ala Ala Gly Ser Gly Met Gly Gly Met Gly Gly Leu Asp
    725                      730                      735
Asp Asp Ile Gly Ser Ser Ala Val Ser Ala Gln Asn Arg Gly Lys Lys
    740                      745                      750
Met Leu Val Lys Glu His Met Gly Gly Gly Gly Gly Lys Asp Asn Asp
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gtg gag gct gag aag tgg gat gac gcc ttc ctg ctg ctg cac gcg cac      143
Val Glu Ala Glu Lys Trp Asp Asp Ala Phe Leu Leu Leu His Ala His
    35                      40                      45

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Pro Glu Cys Arg Gln Asp Val Tyr Leu Pro Tyr Ala Lys Trp Leu Ser
    50                      55                      60

aac cag gac cgc ttc gat gag gcg cgg ctg gcg tac cag gag ggc ggc      239
Asn Gln Asp Arg Phe Asp Glu Ala Arg Leu Ala Tyr Gln Glu Gly Gly
    65                      70                      75

ttt ccc agc ctg gcc acc cgc atc ctg gag cag ttg tgc gcc aac gcg      287
Phe Pro Ser Leu Ala Thr Arg Ile Leu Glu Gln Leu Cys Ala Asn Ala
    80                      85                      90                      95

gtg gta gag acg cgg tac gcg gac gcc gcc ttc tac tac tat cag ctg      335
Val Val Glu Thr Arg Tyr Ala Asp Ala Ala Phe Tyr Tyr Tyr Gln Leu
    100                      105                      110

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gcc gag gtg tac tac gcc tac gaa gtg gtg cac aag tcc gtg cac tcg Ala Glu Val Tyr Tyr Ala Tyr Glu Val Val His Lys Ser Val His Ser 145 150 155	479
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ctg ctc atg cgc ctg ctg ccg ccg cgc gag gtg ccg ctg ggc gtc agc Leu Leu Met Arg Leu Leu Pro Pro Arg Glu Val Pro Leu Gly Val Ser 180 185 190	575
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gcc ggc cgc tgg tgt gag cgg ggt cgc cta tcg ggc gct tac cgg gtg Ala Gly Arg Trp Cys Glu Arg Gly Arg Leu Ser Gly Ala Tyr Arg Val 480 485 490 495	1487
cgt ggg tgg att ccg gat gta ggc ggg gaa taggagctgc cggtagtggc Arg Gly Trp Ile Pro Asp Val Gly Gly Glu 500 505	1537
gttgcagcag gccttcgtta cgcagcagag ggggcacgag gaggacgtga acgggtgtct tcatgctgct tgttgtctga cttggttagga cgggcgttgg tgccatcatt aggctgcccc tgccgggtcca ccataggagc tgcgatgggc ctgaagcaag gcccatgcac ggtggccggg cacatgatgc atgacgggac agagcacggg acttgctgga accagtgtac atatgcccgc gcagagactg cgtgtctcga agcgggcaca aattggggaca tgtcggcgta cagacaaacg atgatgatga caggatgaca gttgttgtgc ggcagggggg ctcccaagcc cagttgaggc ccaggcaggt ttggttgaat ggggatgcac agtggcagtg ctaatgcgct ggcgctatga gcgtccatgg tgttgccggc ctcaagtaca agacacctta tagtagttca atctgccccg caaaaaaaaa aaaaaaaaaa	1597 1657 1717 1777 1837 1897 1957 2017 2036

<210> 18

<211> 505

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 18

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Thr	Leu	Leu	Lys	Met	Asp	Asp	Thr	Lys	Gly	Leu	Ile	Thr	Leu	Tyr	Val
			20					25					30		
Glu	Ala	Glu	Lys	Trp	Asp	Asp	Ala	Phe	Leu	Leu	Leu	His	Ala	His	Pro
		35					40					45			
Glu	Cys	Arg	Gln	Asp	Val	Tyr	Leu	Pro	Tyr	Ala	Lys	Trp	Leu	Ser	Asn
	50					55					60				
Gln	Asp	Arg	Phe	Asp	Glu	Ala	Arg	Leu	Ala	Tyr	Gln	Glu	Gly	Gly	Phe
65					70					75					80
Pro	Ser	Leu	Ala	Thr	Arg	Ile	Leu	Glu	Gln	Leu	Cys	Ala	Asn	Ala	Val
				85					90					95	
Val	Glu	Thr	Arg	Tyr	Ala	Asp	Ala	Ala	Phe	Tyr	Tyr	Tyr	Gln	Leu	Ala
			100					105					110		
Met	Glu	Ala	Leu	Lys	Ser	Ile	Lys	Asn	Pro	Pro	Ser	Asn	Met	Ala	Pro
		115					120					125			
Ser	Asp	Arg	Ser	Ala	Leu	Glu	Arg	Phe	Thr	Glu	Leu	Tyr	Asp	Arg	Ala
	130					135					140				
Glu	Val	Tyr	Tyr	Ala	Tyr	Glu	Val	Val	His	Lys	Ser	Val	His	Ser	Pro
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Phe	Arg	Thr	Thr	His	Pro	Asp	Thr	Leu	Phe	Asn	Ala	Ser	Arg	Phe	Leu
				165					170					175	
Leu	Met	Arg	Leu	Leu	Pro	Pro	Arg	Glu	Val	Pro	Leu	Gly	Val	Ser	Val
		180						185					190		
Val	Asn	Val	Val	Tyr	Val	Leu	Ala	Lys	Gln	Ala	Val	Glu	Ala	Gly	Ala
	195						200					205			
Phe	Lys	Leu	Ala	Arg	Phe	Ala	Tyr	Asn	Lys	Leu	Gln	Thr	Leu	Val	Leu
	210					215					220				
Pro	Ala	Ala	Trp	Gln	Ala	Glu	Val	Asp	Leu	Ala	Ser	Val	Val	Ile	Arg
225				230						235					240
Ser	Lys	Pro	Phe	Ser	Asp	Lys	Glu	Asp	Leu	Leu	Pro	Val	Cys	Trp	Arg
				245				250						255	
Cys	Ser	Thr	Thr	Asn	Pro	Leu	Leu	Asn	Thr	Gln	Gly	Asp	Tyr	Cys	Ile
			260					265					270		
Asn	Cys	Gly	Ala	Pro	Phe	Ile	Arg	Ser	Phe	Val	Thr	Phe	Glu	His	Leu
	275						280					285			
Pro	Val	Val	Glu	Phe	Glu	Leu	Glu	Pro	Gly	Val	Asp	Asp	Glu	Glu	Ala
	290					295					300				
Gly	Arg	Leu	Leu	Gly	Glu	Asp	Ala	Gly	Met	Glu	Ala	Ala	Arg	Arg	Glu
305				310					315						320
Arg	Lys	Ala	Glu	Arg	Gln	Ala	Lys	Ala	Ala	Glu	Val	Gly	Gly	Asn	Met
				325					330					335	
Leu	Arg	Leu	Asp	Gln	Asn	Glu	Ile	Asp	Arg	Met	Asp	Asp	Ala	Phe	Ala
			340					345					350		
Ala	Gln	Met	Met	Val	Pro	Asn	Thr	Thr	Ile	Arg	Val	Asp	Arg	Ala	Met
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Leu	Arg	Arg	Leu	Lys	Thr	Ala	Glu	Val	Met	Val	Arg	Thr	Trp	Pro	Asn
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Pro	Val	Ile	Pro	Lys	Gln	Tyr	Phe	Arg	Ser	His	Gly	Pro	Gly	Gly	Ala
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Ala	Val	Leu	Gln	Asp	Pro	Ala	Asp	Thr	Ser	Ser	Ser	Arg	Met	Ser	Ser
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Arg	Trp	Arg	Arg	Trp	Ser	Val	Ala	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Pro
			420					425					430		
Cys	Ala	Ala	Arg	Ala	Trp	Arg	Arg	Ala	Arg	Thr	Pro	Arg	Met	Arg	Val
		435					440					445			
Pro	Ala	Ala	Thr	Ser	Trp	Ala	Gly	Arg	Trp	Ala	Ala	Arg	Val	Gly	Pro
	450					455					460				
Leu	Gly	Ala	Pro	Ala	Arg	Arg	Ala	Cys	Pro	Cys	Pro	Ser	Ser	Arg	Ala
465					470					475					480
Gly	Arg	Trp	Cys	Glu	Arg	Gly	Arg	Leu	Ser	Gly	Ala	Tyr	Arg	Val	Arg
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Gly	Trp	Ile	Pro	Asp	Val	Gly	Gly	Glu							
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<211> 2602

<212> DNA

<213> Chlamydomonas reinhardtii

<220>

<221> CDS

<222> (236)...(2602)

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ccgtgtatac	acatgctaaa	tatacttcgt	taaattggag	ttcaccgcgg	aggcctgaac	180
atttgccgaa	ccgctcctga	ggaagcagaa	cgaatagcag	tgcatacaaa	tagcc atg	238
					Met	
					1	

gcg gac agg gta ctt gcc ctg gtc cat tac tat gct cgc gag ggc tat	286
Ala Asp Arg Val Leu Ala Leu Val His Tyr Tyr Ala Arg Glu Gly Tyr	
5 10 15	

ttt aga cat gtg cag acg gtg tgc aac gaa gtg ctc aag aag cgg ccg	334
Phe Arg His Val Gln Thr Val Cys Asn Glu Val Leu Lys Lys Arg Pro	
20 25 30	

gga gat ggc gta ctc aca ttc tgg cgt gcc tat gga ctg ctc atg gag	382
Gly Asp Gly Val Leu Thr Phe Trp Arg Ala Tyr Gly Leu Leu Met Glu	
35 40 45	

ggc aac acg gcg gac gcc atg cgt gac ctc tcc agc atc cag ggc aat	430
Gly Asn Thr Ala Asp Ala Met Arg Asp Leu Ser Ser Ile Gln Gly Asn	
50 55 60 65	

tct gac ctt gag ctg gcg gtc gca gcc gcg caa cta ctg ggt cac gaa	478
Ser Asp Leu Glu Leu Ala Val Ala Ala Ala Gln Leu Leu Gly His Glu	
70 75 80	

tcc gcc aag gtg ccc gac cac gat gcc atc att gac ctc caa gcc aag	526
Ser Ala Lys Val Pro Asp His Asp Ala Ile Ile Asp Leu Gln Ala Lys	
85 90 95	

ctg gag atc gag gag cgc acc gcc agc gac cag ccc tgc ctg cac ctg	574
Leu Glu Ile Glu Glu Arg Thr Ala Ser Asp Gln Pro Cys Leu His Leu	
100 105 110	

gcc tcc ttc tac ctg tat acc aag tcc aag gag cgc gcc cgc ggt ctg Ala Ser Phe Tyr Leu Tyr Thr Lys Ser Lys Glu Arg Ala Arg Gly Leu 115 120 125	622
gtg gag cgc gtg ctg cgc aac cag ccc gac atg gtg ccg gcg cag gtt Val Glu Arg Val Leu Arg Asn Gln Pro Asp Met Val Pro Ala Gln Val 130 135 140 145	670
ctt ctg ggc tgg atc atc atc agc cag cag cag gac gac gag tac gac Leu Leu Gly Trp Ile Ile Ile Ser Gln Gln Gln Asp Asp Glu Tyr Asp 150 155 160	718
atg ctg ttt gac gag tcc gag ctg gac gac gcc ctc agc cac ttc gag Met Leu Phe Asp Glu Ser Glu Leu Asp Asp Ala Leu Ser His Phe Glu 165 170 175	766
cag gcg gtg gag cac gac cac aac gac ctg cag gcg ctg ctg ggc aaa Gln Ala Val Glu His Asp His Asn Asp Leu Gln Ala Leu Leu Gly Lys 180 185 190	814
gcc aag atc atg gag ctg aag aag cag ctg ggg ccc tgc ctg gac gtg Ala Lys Ile Met Glu Leu Lys Lys Gln Leu Gly Pro Cys Leu Asp Val 195 200 205	862
ctg acg gag atc aac gtg cgc ttc ggc tgg ttc gtg ccg gcg ctg gtg Leu Thr Glu Ile Asn Val Arg Phe Gly Trp Phe Val Pro Ala Leu Val 210 215 220 225	910
gaa aag acg cgc atg ctc atg atg ctg ggc gac tgg gag cag gtg acg Glu Lys Thr Arg Met Leu Met Met Leu Gly Asp Trp Glu Gln Val Thr 230 235 240	958
gag acg ctg cag cgg gtg ctt gcg gcg gac caa cag aac atc atg gcg Glu Thr Leu Gln Arg Val Leu Ala Ala Asp Gln Gln Asn Ile Met Ala 245 250 255	1006
cag gcc tgg aac tgc atg atc tcc ctc act cgc gag ggc aac aac aag Gln Ala Trp Asn Cys Met Ile Ser Leu Thr Arg Glu Gly Asn Asn Lys 260 265 270	1054
cag gcg gcc aag cag ctg cag gac ctg ttc agc tca atg aac cgc cag Gln Ala Ala Lys Gln Leu Gln Asp Leu Phe Ser Ser Met Asn Arg Gln 275 280 285	1102
gag ccc aag aac gcc gag ctc ttc ttc cgc gtc gcc cgg ccc ttc ggc Glu Pro Lys Asn Ala Glu Leu Phe Phe Arg Val Ala Arg Pro Phe Gly 290 295 300 305	1150
cgc ctg gcc tgc agc gac ccc acg ctg ctg ggc atc acc tac ctc atg Arg Leu Ala Cys Ser Asp Pro Thr Leu Leu Gly Ile Thr Tyr Leu Met 310 315 320	1198
gcc gac cgc gcc gcg cag ctc agg ccg gag atg gcg gcc tac gtg gtg Ala Asp Arg Ala Ala Gln Leu Arg Pro Glu Met Ala Ala Tyr Val Val 325 330 335	1246

gag gca gct gct cag aag ctg atg atg gac gag acc acc aac gcc acg Glu Ala Ala Ala Gln Lys Leu Met Met Asp Glu Thr Thr Asn Ala Thr 340 345 350	1294
gag cgc ttc acg cag gcg cta cag ctg gac gag ctg aac ctg gag gcc Glu Arg Phe Thr Gln Ala Leu Gln Leu Asp Glu Leu Asn Leu Glu Ala 355 360 365	1342
aac gcg ggc gcg ctg gag gcg cag atc atg gcg ggc gag ctg gag gag Asn Ala Gly Ala Leu Glu Ala Gln Ile Met Ala Gly Glu Leu Glu Glu 370 375 380 385	1390
gcg gcg ggg cag atc atg ttc ctg gag gac atg ttc acc aac gcc gcg Ala Ala Gly Gln Ile Met Phe Leu Glu Asp Met Phe Thr Asn Ala Ala 390 395 400	1438
gcg gct ggc ggc ggc aag cgc aag ggc cgc ggc acc ggc gac atg gac Ala Ala Gly Gly Gly Lys Arg Lys Gly Arg Gly Thr Gly Asp Met Asp 405 410 415	1486
gac gac ccc gat atg gcc gac ccc agt ctg ggc acc tcc tcc gac aac Asp Asp Pro Asp Met Ala Asp Pro Ser Leu Gly Thr Ser Ser Asp Asn 420 425 430	1534
ccc acg ctg ctc tac ctc aag ggt ctg ctg gcc tgg aag cag ggc atg Pro Thr Leu Leu Tyr Leu Lys Gly Leu Leu Ala Trp Lys Gln Gly Met 435 440 445	1582
ccg tcc gag ggc ctg ggt ctg ctg gag cgc tcc att gcc gcc ctg ttc Pro Ser Glu Gly Leu Gly Leu Leu Glu Arg Ser Ile Ala Ala Leu Phe 450 455 460 465	1630
tcc gcc gcc gcc gac ttc cac ggc ccc agc ctg gag ctg tac gcg gcg Ser Ala Ala Ala Asp Phe His Gly Pro Ser Leu Glu Leu Tyr Ala Ala 470 475 480	1678
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agc aag gtc acc cgc gcg ctg gac ctg ctg aac aag cag gcg ccg gcg Ser Lys Val Thr Arg Ala Leu Asp Leu Leu Asn Lys Gln Ala Pro Ala 515 520 525	1822
ctg cag gag agc gcg ctg ctg cac gcg cgc gcg ctg tac ctg aac ggc Leu Gln Glu Ser Ala Leu Leu His Ala Arg Ala Leu Tyr Leu Asn Gly 530 535 540 545	1870
aac ctg gac ggc gcg ctg cgc aag gcg ggc gag atc ctg cgc atg aac Asn Leu Asp Gly Ala Leu Arg Lys Ala Gly Glu Ile Leu Arg Met Asn 550 555 560	1918

ccc gag gag agc tcc gcg cac ctg ctc atc tgt tcc gtg tac gtg gcg Pro Glu Glu Ser Ser Ala His Leu Leu Ile Cys Ser Val Tyr Val Ala 565 570 575	1966
cag gac aag ccc gag ctg gcc gtc agc gcg ctg gac cag gcc gtc agc Gln Asp Lys Pro Glu Leu Ala Val Ser Ala Leu Asp Gln Ala Val Ser 580 585 590	2014
agc aac ttc gcg atc cgc gag acg cct ctg tac cac gtg gtc cag gcc Ser Asn Phe Ala Ile Arg Glu Thr Pro Leu Tyr His Val Val Gln Ala 595 600 605	2062
aag gtg ctg gtg gcc aac aac aag ctg gac gac gcc aag cgc gtc ctg Lys Val Leu Val Ala Asn Asn Lys Leu Asp Asp Ala Lys Arg Val Leu 610 615 620 625	2110
gag tcc gcc atg aac ctg ccg ggc gtg cgc aca gcg ctc acc gtg cag Glu Ser Ala Met Asn Leu Pro Gly Val Arg Thr Ala Leu Thr Val Gln 630 635 640	2158
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cgc gcc acc gtg tac ctg ctg ctg gcg gac gtg ctg gcg agg cag tcc Arg Ala Thr Val Tyr Leu Leu Leu Ala Asp Val Leu Ala Arg Gln Ser 660 665 670	2254
aag ata ccg gac gca cca gag gcc aag aag tac atc caa gac gcc atc Lys Ile Pro Asp Ala Pro Glu Ala Lys Lys Tyr Ile Gln Asp Ala Ile 675 680 685	2302
cgc gag ttc gag ggc acc agc gag gag gtg cgc gtc acg gtg gcg gac Arg Glu Phe Glu Gly Thr Ser Glu Glu Val Arg Val Thr Val Ala Asp 690 695 700 705	2350
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ctg cgg cgc atc ccc aag gag tct ccg cac tac gtg aag gcg cgc atg Leu Arg Arg Ile Pro Lys Glu Ser Pro His Tyr Val Lys Ala Arg Met 725 730 735	2446
gcc atg gcc gac atc tac ctg cgc cac cgc aag gac aag gcc gcc tac Ala Met Ala Asp Ile Tyr Leu Arg His Arg Lys Asp Lys Ala Ala Tyr 740 745 750	2494
atc aag tgc tac atg gac ctg gtg gac cac acg ccc gac tac gac agc Ile Lys Cys Tyr Met Asp Leu Val Asp His Thr Pro Asp Tyr Asp Ser 755 760 765	2542
tac tgc atg ctg ggc gag gcg ttc atg cag atc cag gag ccg gag aag Tyr Cys Met Leu Gly Glu Ala Phe Met Gln Ile Gln Glu Pro Glu Lys 770 775 780 785	2590

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Ala Val Arg Ala

2602

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<211> 789
<212> PRT
<213> Chlamydomonas reinhardtii

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Tyr Phe Arg His Val Gln Thr Val Cys Asn Glu Val Leu Lys Lys Arg
20 25 30
Pro Gly Asp Gly Val Leu Thr Phe Trp Arg Ala Tyr Gly Leu Leu Met
35 40 45
Glu Gly Asn Thr Ala Asp Ala Met Arg Asp Leu Ser Ser Ile Gln Gly
50 55 60
Asn Ser Asp Leu Glu Leu Ala Val Ala Ala Ala Gln Leu Leu Gly His
65 70 75 80
Glu Ser Ala Lys Val Pro Asp His Asp Ala Ile Ile Asp Leu Gln Ala
85 90 95
Lys Leu Glu Ile Glu Glu Arg Thr Ala Ser Asp Gln Pro Cys Leu His
100 105 110
Leu Ala Ser Phe Tyr Leu Tyr Thr Lys Ser Lys Glu Arg Ala Arg Gly
115 120 125
Leu Val Glu Arg Val Leu Arg Asn Gln Pro Asp Met Val Pro Ala Gln
130 135 140
Val Leu Leu Gly Trp Ile Ile Ile Ser Gln Gln Gln Asp Asp Glu Tyr
145 150 155 160
Asp Met Leu Phe Asp Glu Ser Glu Leu Asp Asp Ala Leu Ser His Phe
165 170 175
Glu Gln Ala Val Glu His Asp His Asn Asp Leu Gln Ala Leu Leu Gly
180 185 190
Lys Ala Lys Ile Met Glu Leu Lys Lys Gln Leu Gly Pro Cys Leu Asp
195 200 205
Val Leu Thr Glu Ile Asn Val Arg Phe Gly Trp Phe Val Pro Ala Leu
210 215 220
Val Glu Lys Thr Arg Met Leu Met Met Leu Gly Asp Trp Glu Gln Val
225 230 235 240
Thr Glu Thr Leu Gln Arg Val Leu Ala Ala Asp Gln Gln Asn Ile Met
245 250 255
Ala Gln Ala Trp Asn Cys Met Ile Ser Leu Thr Arg Glu Gly Asn Asn
260 265 270
Lys Gln Ala Ala Lys Gln Leu Gln Asp Leu Phe Ser Ser Met Asn Arg
275 280 285
Gln Glu Pro Lys Asn Ala Glu Leu Phe Phe Arg Val Ala Arg Pro Phe
290 295 300
Gly Arg Leu Ala Cys Ser Asp Pro Thr Leu Leu Gly Ile Thr Tyr Leu
305 310 315 320
Met Ala Asp Arg Ala Ala Gln Leu Arg Pro Glu Met Ala Ala Tyr Val
325 330 335
Val Glu Ala Ala Ala Gln Lys Leu Met Met Asp Glu Thr Thr Asn Ala
340 345 350
Thr Glu Arg Phe Thr Gln Ala Leu Gln Leu Asp Glu Leu Asn Leu Glu
355 360 365

Ala	Asn	Ala	Gly	Ala	Leu	Glu	Ala	Gln	Ile	Met	Ala	Gly	Glu	Leu	Glu
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Glu	Ala	Ala	Gly	Gln	Ile	Met	Phe	Leu	Glu	Asp	Met	Phe	Thr	Asn	Ala
385					390					395					400
Ala	Ala	Ala	Gly	Gly	Gly	Lys	Arg	Lys	Gly	Arg	Gly	Thr	Gly	Asp	Met
			405						410					415	
Asp	Asp	Asp	Pro	Asp	Met	Ala	Asp	Pro	Ser	Leu	Gly	Thr	Ser	Ser	Asp
			420					425					430		
Asn	Pro	Thr	Leu	Leu	Tyr	Leu	Lys	Gly	Leu	Leu	Ala	Trp	Lys	Gln	Gly
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Met	Pro	Ser	Glu	Gly	Leu	Gly	Leu	Leu	Glu	Arg	Ser	Ile	Ala	Ala	Leu
	450					455					460				
Phe	Ser	Ala	Ala	Ala	Asp	Phe	His	Gly	Pro	Ser	Leu	Glu	Leu	Tyr	Ala
465					470					475					480
Ala	Leu	Asn	Pro	Ala	Arg	Ile	Thr	Ala	Met	Val	Arg	Leu	Leu	Leu	Gln
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Ser	Ile	Gly	Gly	Glu	Pro	Arg	Ala	Pro	Thr	Glu	Ala	Pro	Ser	Pro	Leu
			500					505					510		
Ile	Ser	Lys	Val	Thr	Arg	Ala	Leu	Asp	Leu	Leu	Asn	Lys	Gln	Ala	Pro
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Ala	Leu	Gln	Glu	Ser	Ala	Leu	Leu	His	Ala	Arg	Ala	Leu	Tyr	Leu	Asn
	530					535					540				
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Asn	Pro	Glu	Glu	Ser	Ser	Ala	His	Leu	Leu	Ile	Cys	Ser	Val	Tyr	Val
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Ser	Ser	Asn	Phe	Ala	Ile	Arg	Glu	Thr	Pro	Leu	Tyr	His	Val	Val	Gln
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625					630					635					640
Gln	Gln	Arg	Ala	Arg	Leu	Gly	Arg	Lys	Val	Val	Glu	Pro	Thr	Leu	His
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Glu	Arg	Ala	Thr	Val	Tyr	Leu	Leu	Leu	Ala	Asp	Val	Leu	Ala	Arg	Gln
			660					665					670		
Ser	Lys	Ile	Pro	Asp	Ala	Pro	Glu	Ala	Lys	Lys	Tyr	Ile	Gln	Asp	Ala
		675					680					685			
Ile	Arg	Glu	Phe	Glu	Gly	Thr	Ser	Glu	Glu	Val	Arg	Val	Thr	Val	Ala
	690					695					700				
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705					710				715						720
Lys	Leu	Arg	Arg	Ile	Pro	Lys	Glu	Ser	Pro	His	Tyr	Val	Lys	Ala	Arg
				725					730					735	
Met	Ala	Met	Ala	Asp	Ile	Tyr	Leu	Arg	His	Arg	Lys	Asp	Lys	Ala	Ala
			740					745					750		
Tyr	Ile	Lys	Cys	Tyr	Met	Asp	Leu	Val	Asp	His	Thr	Pro	Asp	Tyr	Asp
		755					760					765			
Ser	Tyr	Cys	Met	Leu	Gly	Glu	Ala	Phe	Met	Gln	Ile	Gln	Glu	Pro	Glu
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<212> DNA

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<221> CDS

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Thr Ala Ala Val Gly Trp Asn Val Trp Asn Glu Leu Phe Thr Cys Ser	
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gac gac cag act att cac aaa tgg aac atg ctg ggg gag cca gag cag	144
Asp Asp Gln Thr Ile His Lys Trp Asn Met Leu Gly Glu Pro Glu Gln	
35 40 45	
aag gtc agc act ctg gac gca tac ttc acg gat atg cac tgg tac ccc	192
Lys Val Ser Thr Leu Asp Ala Tyr Phe Thr Asp Met His Trp Tyr Pro	
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Val Ser Ser Lys Lys Trp Gln Ala Gly Gly Thr Asp Val Phe Ala Val	
65 70 75 80	
gcg tgc aca gac ggc tct gta aaa atc ctc agc cgc acg ggc cgc gtg	288
Ala Cys Thr Asp Gly Ser Val Lys Ile Leu Ser Arg Thr Gly Arg Val	
85 90 95	
gag aag tcc att gag ggg cac aag ggc gcg tgc atc tcg ctg cgc tgg	336
Glu Lys Ser Ile Glu Gly His Lys Gly Ala Cys Ile Ser Leu Arg Trp	
100 105 110	
agc tat gac ggg acg gca ctg gcg acg gcg ggc gag gac ggg tcg gta	384
Ser Tyr Asp Gly Thr Ala Leu Ala Thr Ala Gly Glu Asp Gly Ser Val	
115 120 125	
aag atc tgg tcg cgc aac ggc atg ctg cgc tcc acg cta gcg cag gcg	432
Lys Ile Trp Ser Arg Asn Gly Met Leu Arg Ser Thr Leu Ala Gln Ala	
130 135 140	
gac agc ccc gtg tac tcg att gtg tgg gcc tac gac tgc gac cag ctg	480
Asp Ser Pro Val Tyr Ser Ile Val Trp Ala Tyr Asp Cys Asp Gln Leu	
145 150 155 160	
tgc tac tgc acc ggc tcc aac gtg gtc atc aag tcg ctg tcc tcc aac	528
Cys Tyr Cys Thr Gly Ser Asn Val Val Ile Lys Ser Leu Ser Ser Asn	
165 170 175	
gcc aag cag aac gcg tgg aag gcg cac gac ggc gtg gtg ctc aag gtg	576
Ala Lys Gln Asn Ala Trp Lys Ala His Asp Gly Val Val Leu Lys Val	
180 185 190	

gac tgg agc ccc atc aac cac ctc atc atc aca ggc ggc gag gac tgc Asp Trp Ser Pro Ile Asn His Leu Ile Ile Thr Gly Gly Glu Asp Cys 195 200 205	624
aag tac aag gtg tgg gac agc ttt ggg cgg ctg ctg ttc cag agc ggg Lys Tyr Lys Val Trp Asp Ser Phe Gly Arg Leu Leu Phe Gln Ser Gly 210 215 220	672
ctg ttc gac tac ccg gtc acg tcg gtg gcg tgg gcg ccc agc ggc gag Leu Phe Asp Tyr Pro Val Thr Ser Val Ala Trp Ala Pro Ser Gly Glu 225 230 235 240	720
ctg ttc gcg gtg ggc ggc ttc aac acg ctg cag ctg tgt gac cgc atg Leu Phe Ala Val Gly Gly Phe Asn Thr Leu Gln Leu Cys Asp Arg Met 245 250 255	768
ggc tgg gcc tac tcc aag atc cac ctc aac gac acg ggc agc atc atg Gly Trp Ala Tyr Ser Lys Ile His Leu Asn Asp Thr Gly Ser Ile Met 260 265 270	816
act ctg agc tgg acg gcg gac agc acg cag ctg gcg ggc ggc ggc ggc Thr Leu Ser Trp Thr Ala Asp Ser Thr Gln Leu Ala Gly Gly Gly Gly 275 280 285	864
agc ggc ggc gtg gtg ttc ggc cag gtg gtg gac ctg gcg ctg gag gac Ser Gly Gly Val Val Phe Gly Gln Val Val Asp Leu Ala Leu Glu Asp 290 295 300	912
ggc aag atg cag gtg acg gtg gtg gac gac atg cgc att gtg gtg aac Gly Lys Met Gln Val Thr Val Val Asp Asp Met Arg Ile Val Val Asn 305 310 315 320	960
gac atc ttg aac gag aac gcg gac gag ctg ccc gag ttc cgt gac cgc Asp Ile Leu Asn Glu Asn Ala Asp Glu Leu Pro Glu Phe Arg Asp Arg 325 330 335	1008
gtc atc aag gtg tcg cta ggg tac ggc tac ctg atc gtg gcc acc gcg Val Ile Lys Val Ser Leu Gly Tyr Gly Tyr Leu Ile Val Ala Thr Ala 340 345 350	1056
acg cag tgc cac gtg tac aac acc acc aac ctg ggc acg ccg cac atc Thr Gln Cys His Val Tyr Asn Thr Thr Asn Leu Gly Thr Pro His Ile 355 360 365	1104
ttt gac ctc aaa gac acg gtc acc ctg ctg ctg cag gct gag cgg cac Phe Asp Leu Lys Asp Thr Val Thr Leu Leu Leu Gln Ala Glu Arg His 370 375 380	1152
ttc ctg ctg ctg gac aac tcg gcg ggc atc cag atc tac acc tac gag Phe Leu Leu Leu Asp Asn Ser Ala Gly Ile Gln Ile Tyr Thr Tyr Glu 385 390 395 400	1200
ggc cgc cag atc tgc aac ccg cgc ttc cag ggc ctg cgc acc gag ctg Gly Arg Gln Ile Cys Asn Pro Arg Phe Gln Gly Leu Arg Thr Glu Leu 405 410 415	1248

ctg aac gcg cag atg atc acg ctg tcc aac gac acg ata gcg gtg ctg Leu Asn Ala Gln Met Ile Thr Leu Ser Asn Asp Thr Ile Ala Val Leu 420 425 430	1296
gac cag cag gcc agc ggc acc acc gtg cgc ttc ttc gac acg gcg cag Asp Gln Gln Ala Ser Gly Thr Thr Val Arg Phe Phe Asp Thr Ala Gln 435 440 445	1344
ggc cgg cca gtg ggc gag ccg tgg cag cac acg ttg gag gtg aag gag Gly Arg Pro Val Gly Glu Pro Trp Gln His Thr Leu Glu Val Lys Glu 450 455 460	1392
atc gcg ctg agc cag gcc ggc acc atc aac gac cgc cag ctc atc gtc Ile Ala Leu Ser Gln Ala Gly Thr Ile Asn Asp Arg Gln Leu Ile Val 465 470 475 480	1440
atc gac cgc aac cgc gac ctg tac ctg ctg ccc gtc atg aag cgc cac Ile Asp Arg Asn Arg Asp Leu Tyr Leu Leu Pro Val Met Lys Arg His 485 490 495	1488
gtg gcc aag ctg gcg gcc atg tgc gac tcg gcg cgc tgg cac gac agc Val Ala Lys Leu Ala Ala Met Cys Asp Ser Ala Arg Trp His Asp Ser 500 505 510	1536
acc gcc atg ctg tcc gcc atg gtg gac cag cgc ctg tgt gtg tgg tac Thr Ala Met Leu Ser Ala Met Val Asp Gln Arg Leu Cys Val Trp Tyr 515 520 525	1584
tac ccc agc gag gtg tac gtg gac aag gac ctg ctg gcc aag acg cgc Tyr Pro Ser Glu Val Tyr Val Asp Lys Asp Leu Leu Ala Lys Thr Arg 530 535 540	1632
tac acc aag tcc gac tcg gac ttt ggc aag tcg gcc cag atc cag ctc Tyr Thr Lys Ser Asp Ser Asp Phe Gly Lys Ser Ala Gln Ile Gln Leu 545 550 555 560	1680
ttc gcc ggc aac cgc tgc ctg gtg cgc cgc tcc gac ggc gtg ctg gtc Phe Ala Gly Asn Arg Cys Leu Val Arg Arg Ser Asp Gly Val Leu Val 565 570 575	1728
tcc gcc gcc acc tcg ccc tac cct gcc gta ctg tac gac atg atc cgc Ser Ala Ala Thr Ser Pro Tyr Pro Ala Val Leu Tyr Asp Met Ile Arg 580 585 590	1776
aag cag cag tgg gac aag gcc acg cgg ctg tgt cgc ttc atc aag gac Lys Gln Gln Trp Asp Lys Ala Thr Arg Leu Cys Arg Phe Ile Lys Asp 595 600 605	1824
ccc acc atg tgg gcc acg ctg gcg gcg atg gcc atg gcg gct aag gag Pro Thr Met Trp Ala Thr Leu Ala Ala Met Ala Met Ala Ala Lys Glu 610 615 620	1872
ctg aac acg gcg gag gtg gcg ttc gcg gcg att gac gag gtg gac aaa Leu Asn Thr Ala Glu Val Ala Phe Ala Ala Ile Asp Glu Val Asp Lys 625 630 635 640	1920

acg cac ttt gtg cgc aag gtg aag cag atc ccc acg gag gag ggc cgc	1968
Thr His Phe Val Arg Lys Val Lys Gln Ile Pro Thr Glu Glu Gly Arg	
645 650 655	
aac gcc gag ctg gcg gtg tac cgg cgc aag ccc gag gag ggc gag tcc	2016
Asn Ala Glu Leu Ala Val Tyr Arg Arg Lys Pro Glu Glu Gly Glu Ser	
660 665 670	
ata ctg ctg cag gcc ggc ctg gtc ttc cgc gcc atc aag ctg aac atc	2064
Ile Leu Leu Gln Ala Gly Leu Val Phe Arg Ala Ile Lys Leu Asn Ile	
675 680 685	
aag ctg ttc aac tgg gag cgc gcg ctg sac ctg gcc acg cag cac aag	2112
Lys Leu Phe Asn Trp Glu Arg Ala Leu Xaa Leu Ala Thr Gln His Lys	
690 695 700	
cag cac cag gac acg gtg ctg tgg tac cgc cag cag ttc ctc aag aac	2160
Gln His Gln Asp Thr Val Leu Trp Tyr Arg Gln Gln Phe Leu Lys Asn	
705 710 715 720	
gcc aag ctc gcc gag tcc atc acg cgc ttc atg cag atg aac gag tcg	2208
Ala Lys Leu Ala Glu Ser Ile Thr Arg Phe Met Gln Met Asn Glu Ser	
725 730 735	
gtg gtt gtg gac cag gcg gcg gtg aag aag aag atc gag gag gag cgc	2256
Val Val Val Asp Gln Ala Ala Val Lys Lys Lys Ile Glu Glu Glu Arg	
740 745 750	
atc aag gag tcg cag cgg cca ggc gcc aag cgc tac gtg taa	2298
Ile Lys Glu Ser Gln Arg Pro Gly Ala Lys Arg Tyr Val	
755 760 765	

<210> 22
 <211> 765
 <212> PRT
 <213> Chlamydomonas reinhardtii

<220>
 <221> VARIANT
 <222> (1)...(765)
 <223> Xaa = Any Amino Acid

<400> 22	
Met Arg Leu Lys Val Lys Gln Ser Ser Ala Asn Val His Ser Glu Leu	
1 5 10 15	
Thr Ala Ala Val Gly Trp Asn Val Trp Asn Glu Leu Phe Thr Cys Ser	
20 25 30	
Asp Asp Gln Thr Ile His Lys Trp Asn Met Leu Gly Glu Pro Glu Gln	
35 40 45	
Lys Val Ser Thr Leu Asp Ala Tyr Phe Thr Asp Met His Trp Tyr Pro	
50 55 60	
Val Ser Ser Lys Lys Thr Gln Ala Gly Gly Thr Asp Val Phe Ala Val	
65 70 75 80	
Ala Cys Thr Asp Gly Ser Val Lys Ile Leu Ser Arg Thr Gly Arg Val	
85 90 95	

Glu	Lys	Ser	Ile	Glu	Gly	His	Lys	Gly	Ala	Cys	Ile	Ser	Leu	Arg	Trp
			100					105					110		
Ser	Tyr	Asp	Gly	Thr	Ala	Leu	Ala	Thr	Ala	Gly	Glu	Asp	Gly	Ser	Val
		115					120					125			
Lys	Ile	Trp	Ser	Arg	Asn	Gly	Met	Leu	Arg	Ser	Thr	Leu	Ala	Gln	Ala
		130				135					140				
Asp	Ser	Pro	Val	Tyr	Ser	Ile	Val	Trp	Ala	Tyr	Asp	Cys	Asp	Gln	Leu
145					150					155					160
Cys	Tyr	Cys	Thr	Gly	Ser	Asn	Val	Val	Ile	Lys	Ser	Leu	Ser	Ser	Asn
				165					170						175
Ala	Lys	Gln	Asn	Ala	Trp	Lys	Ala	His	Asp	Gly	Val	Val	Leu	Lys	Val
			180					185					190		
Asp	Trp	Ser	Pro	Ile	Asn	His	Leu	Ile	Ile	Thr	Gly	Gly	Glu	Asp	Cys
		195					200					205			
Lys	Tyr	Lys	Val	Trp	Asp	Ser	Phe	Gly	Arg	Leu	Leu	Phe	Gln	Ser	Gly
		210				215					220				
Leu	Phe	Asp	Tyr	Pro	Val	Thr	Ser	Val	Ala	Trp	Ala	Pro	Ser	Gly	Glu
225					230					235					240
Leu	Phe	Ala	Val	Gly	Gly	Phe	Asn	Thr	Leu	Gln	Leu	Cys	Asp	Arg	Met
				245					250					255	
Gly	Trp	Ala	Tyr	Ser	Lys	Ile	His	Leu	Asn	Asp	Thr	Gly	Ser	Ile	Met
			260					265					270		
Thr	Leu	Ser	Trp	Thr	Ala	Asp	Ser	Thr	Gln	Leu	Ala	Gly	Gly	Gly	Gly
		275					280					285			
Ser	Gly	Gly	Val	Val	Phe	Gly	Gln	Val	Val	Asp	Leu	Ala	Leu	Glu	Asp
	290					295					300				
Gly	Lys	Met	Gln	Val	Thr	Val	Val	Asp	Asp	Met	Arg	Ile	Val	Val	Asn
305				310						315					320
Asp	Ile	Leu	Asn	Glu	Asn	Ala	Asp	Glu	Leu	Pro	Glu	Phe	Arg	Asp	Arg
			325					330						335	
Val	Ile	Lys	Val	Ser	Leu	Gly	Tyr	Gly	Tyr	Leu	Ile	Val	Ala	Thr	Ala
			340					345					350		
Thr	Gln	Cys	His	Val	Tyr	Asn	Thr	Thr	Asn	Leu	Gly	Thr	Pro	His	Ile
		355					360					365			
Phe	Asp	Leu	Lys	Asp	Thr	Val	Thr	Leu	Leu	Leu	Gln	Ala	Glu	Arg	His
	370					375					380				
Phe	Leu	Leu	Leu	Asp	Asn	Ser	Ala	Gly	Ile	Gln	Ile	Tyr	Thr	Tyr	Glu
385				390						395					400
Gly	Arg	Gln	Ile	Cys	Asn	Pro	Arg	Phe	Gln	Gly	Leu	Arg	Thr	Glu	Leu
			405					410						415	
Leu	Asn	Ala	Gln	Met	Ile	Thr	Leu	Ser	Asn	Asp	Thr	Ile	Ala	Val	Leu
			420					425					430		
Asp	Gln	Gln	Ala	Ser	Gly	Thr	Thr	Val	Arg	Phe	Phe	Asp	Thr	Ala	Gln
		435					440					445			
Gly	Arg	Pro	Val	Gly	Glu	Pro	Trp	Gln	His	Thr	Leu	Glu	Val	Lys	Glu
		450				455					460				
Ile	Ala	Leu	Ser	Gln	Ala	Gly	Thr	Ile	Asn	Asp	Arg	Gln	Leu	Ile	Val
465				470						475					480
Ile	Asp	Arg	Asn	Arg	Asp	Leu	Tyr	Leu	Leu	Pro	Val	Met	Lys	Arg	His
			485					490						495	
Val	Ala	Lys	Leu	Ala	Ala	Met	Cys	Asp	Ser	Ala	Arg	Trp	His	Asp	Ser
			500					505					510		
Thr	Ala	Met	Leu	Ser	Ala	Met	Val	Asp	Gln	Arg	Leu	Cys	Val	Trp	Tyr
		515					520					525			
Tyr	Pro	Ser	Glu	Val	Tyr	Val	Asp	Lys	Asp	Leu	Leu	Ala	Lys	Thr	Arg
	530					535					540				

Tyr Thr Lys Ser Asp Ser Asp Phe Gly Lys Ser Ala Gln Ile Gln Leu
 545 550 555 560
 Phe Ala Gly Asn Arg Cys Leu Val Arg Arg Ser Asp Gly Val Leu Val
 565 570 575
 Ser Ala Ala Thr Ser Pro Tyr Pro Ala Val Leu Tyr Asp Met Ile Arg
 580 585 590
 Lys Gln Gln Trp Asp Lys Ala Thr Arg Leu Cys Arg Phe Ile Lys Asp
 595 600 605
 Pro Thr Met Trp Ala Thr Leu Ala Ala Met Ala Met Ala Ala Lys Glu
 610 615 620
 Leu Asn Thr Ala Glu Val Ala Phe Ala Ala Ile Asp Glu Val Asp Lys
 625 630 635 640
 Thr His Phe Val Arg Lys Val Lys Gln Ile Pro Thr Glu Glu Gly Arg
 645 650 655
 Asn Ala Glu Leu Ala Val Tyr Arg Arg Lys Pro Glu Glu Gly Glu Ser
 660 665 670
 Ile Leu Leu Gln Ala Gly Leu Val Phe Arg Ala Ile Lys Leu Asn Ile
 675 680 685
 Lys Leu Phe Asn Trp Glu Arg Ala Leu Xaa Leu Ala Thr Gln His Lys
 690 695 700
 Gln His Gln Asp Thr Val Leu Trp Tyr Arg Gln Gln Phe Leu Lys Asn
 705 710 715 720
 Ala Lys Leu Ala Glu Ser Ile Thr Arg Phe Met Gln Met Asn Glu Ser
 725 730 735
 Val Val Val Asp Gln Ala Ala Val Lys Lys Lys Ile Glu Glu Glu Arg
 740 745 750
 Ile Lys Glu Ser Gln Arg Pro Gly Ala Lys Arg Tyr Val
 755 760 765

<210> 23
 <211> 132
 <212> PRT
 <213> Homo sapiens

Sub
 QH
 <400> 23
 Met Ala Lys Asp Ile Leu Gly Glu Ala Gly Leu His Phe Asp Glu Leu
 1 5 10 15
 Asn Lys Leu Arg Val Leu Asp Pro Glu Val Thr Gln Gln Thr Ile Glu
 20 25 30
 Leu Lys Glu Glu Cys Lys Asp Phe Val Asp Lys Ile Gly Gln Phe Gln
 35 40 45
 Lys Ile Val Gly Gly Leu Ile Glu Leu Val Asp Gln Leu Ala Lys Glu
 50 55 60
 Ala Glu Asn Glu Lys Met Lys Ala Ile Gly Ala Arg Asn Leu Leu Lys
 65 70 75 80
 Ser Ile Ala Lys Gln Arg Glu Ala Gln Gln Gln Gln Leu Gln Ala Leu
 85 90 95
 Ile Ala Glu Lys Lys Met Gln Leu Glu Arg Tyr Arg Val Glu Tyr Glu
 100 105 110
 Ala Leu Cys Lys Val Glu Ala Glu Gln Asn Glu Phe Ile Asp Gln Phe
 115 120 125
 Ile Phe Gln Lys
 130

<210> 24
 <211> 109

<212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(109)
 <223> Xaa = Unknown (including no amino acid)

<400> 24
 Gln Asp Ser Leu Gly Glu Ala Gly Leu Cys Phe Asp Glu Leu Ser Lys
 1 5 10 15
 Val Arg Asp Pro Glu Val Thr Xaa Gln Thr Arg Asp Pro Lys Glu Asp
 20 25 30
 Cys Met Asp Phe Val Gly Lys Ile Ser Pro Phe Gln Lys Glu Ile Val
 35 40 45
 Gly Gly Leu Ile Glu Pro Val Asp Gln Leu Ala Lys Ala Ala Glu Asn
 50 55 60
 Glu Lys Arg Lys Val Val Gly Ala Trp Asn Leu Leu Gln Phe Met Ala
 65 70 75 80
 Lys His Arg Glu Ala Gln Gln Gln Gln Leu Leu Ala Gln Thr Ala Glu
 85 90 95
 Glu Lys Met Trp Leu Lys Arg Trp Trp Ile Glu Tyr Glu
 100 105

<210> 25
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(76)
 <223> Xaa = Unknown (including no amino acid)

<400> 25
 Met Val Lys Asp Ile Leu Ala Glu Glu Gly Leu His Phe Asp Glu Leu
 1 5 10 15
 Asn Lys Leu Trp Val Leu Asp Ser Glu Val Thr Gln Gln Thr Thr Glu
 20 25 30
 Leu Lys Glu Glu Cys Lys Asn Phe Ala Asp Lys Thr Gly Gln Phe Gln
 35 40 45
 Lys Thr Val Gly Gly Leu Ile Glu Leu Val Asp Lys Leu Ala Lys Lys
 50 55 60
 Ala Xaa Asn Ala Lys Met Arg Ala Met Val Leu Arg
 65 70 75

<210> 26
 <211> 186
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Val Lys Leu Ala Ala Lys Cys Ile Leu Ala Gly Asp Pro Ala Val
 1 5 10 15
 Gly Lys Thr Ala Leu Ala Gln Ile Phe Arg Ser Asp Gly Ala His Phe
 20 25 30

Gln	Lys	Ser	Tyr	Thr	Leu	Thr	Thr	Gly	Met	Asp	Leu	Val	Val	Lys	Thr
		35					40					45			
Val	Pro	Val	Pro	Asp	Thr	Gly	Asp	Ser	Val	Glu	Leu	Phe	Ile	Phe	Asp
	50					55					60				
Ser	Ala	Gly	Lys	Glu	Leu	Phe	Ser	Glu	Met	Leu	Asp	Lys	Leu	Trp	Glu
65					70					75					80
Ser	Pro	Asn	Val	Leu	Cys	Leu	Val	Tyr	Asp	Val	Thr	Asn	Glu	Glu	Ser
			85					90					95		
Phe	Asn	Asn	Cys	Ser	Lys	Trp	Leu	Glu	Lys	Ala	Arg	Ser	Gln	Ala	Pro
			100					105					110		
Gly	Ile	Ser	Leu	Pro	Gly	Val	Leu	Val	Gly	Asn	Lys	Thr	Asp	Leu	Ala
	115					120						125			
Gly	Arg	Arg	Ala	Val	Asp	Ser	Ala	Glu	Ala	Arg	Ala	Trp	Ala	Leu	Gly
130					135						140				
Gln	Gly	Leu	Glu	Cys	Phe	Glu	Thr	Ser	Val	Lys	Glu	Met	Glu	Asn	Phe
145					150					155					160
Glu	Ala	Pro	Phe	His	Cys	Leu	Ala	Lys	Gln	Phe	His	Gln	Leu	Tyr	Arg
				165				170						175	
Glu	Lys	Val	Glu	Val	Phe	Arg	Ala	Leu	Ala						
			180					185							

<210> 27
 <211> 304
 <212> PRT
 <213> Homo sapiens

<400> 27

Met	Ala	Asp	Asn	Ser	Ser	Asp	Glu	Cys	Glu	Glu	Glu	Asn	Asn	Lys	Glu
1				5					10					15	
Lys	Lys	Lys	Thr	Ser	Gln	Leu	Thr	Pro	Gln	Arg	Gly	Phe	Ser	Glu	Asn
			20					25					30		
Glu	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Ser	Ser	Glu	Thr	Asp	Ser	Asp
	35						40					45			
Ser	Asp	Asp	Asp	Asp	Glu	Glu	His	Gly	Ala	Pro	Leu	Glu	Gly	Ala	Tyr
50					55						60				
Asp	Pro	Ala	Asp	Tyr	Glu	His	Leu	Pro	Val	Ser	Ala	Glu	Ile	Lys	Glu
65					70					75					80
Leu	Phe	Gln	Tyr	Ile	Ser	Arg	Tyr	Thr	Pro	Gln	Leu	Ile	Asp	Leu	Asp
				85				90					95		
His	Lys	Leu	Lys	Pro	Phe	Ile	Pro	Asp	Phe	Ile	Pro	Ala	Val	Gly	Asp
			100					105					110		
Ile	Asp	Ala	Phe	Leu	Lys	Val	Pro	Arg	Pro	Asp	Gly	Lys	Pro	Asp	Asn
	115					120					125				
Leu	Gly	Leu	Leu	Val	Leu	Asp	Glu	Pro	Ser	Thr	Lys	Gln	Ser	Asp	Pro
130					135						140				
Thr	Val	Leu	Ser	Leu	Trp	Leu	Thr	Glu	Asn	Ser	Lys	Gln	His	Asn	Ile
145					150					155					160
Thr	Gln	His	Met	Lys	Val	Lys	Ser	Leu	Glu	Asp	Ala	Glu	Lys	Asn	Pro
				165				170						175	
Lys	Ala	Ile	Asp	Thr	Trp	Ile	Glu	Ser	Ile	Ser	Glu	Leu	His	Arg	Ser
			180				185						190		
Lys	Pro	Pro	Ala	Thr	Val	His	Tyr	Thr	Arg	Pro	Met	Pro	Asp	Ile	Asp
	195						200					205			
Thr	Leu	Met	Gln	Glu	Trp	Ser	Pro	Glu	Phe	Glu	Glu	Leu	Leu	Gly	Lys
210					215					220					
Val	Ser	Leu	Pro	Thr	Ala	Glu	Ile	Asp	Cys	Ser	Leu	Ala	Glu	Tyr	Ile
225					230					235					240

Asp	Met	Ile	Cys	Ala	Ile	Leu	Asp	Ile	Pro	Val	Tyr	Lys	Ser	Arg	Ile
				245					250					255	
Gln	Ser	Leu	His	Leu	Leu	Phe	Ser	Leu	Tyr	Ser	Glu	Phe	Lys	Asn	Ser
			260					265					270		
Gln	His	Phe	Lys	Ala	Leu	Ala	Glu	Gly	Lys	Lys	Ala	Phe	Thr	Pro	Ser
		275					280					285			
Ser	Asn	Ser	Thr	Ser	Gln	Ala	Gly	Asp	Met	Glu	Thr	Leu	Thr	Phe	Ser
	290					295					300				

<210> 28

<211> 438

<212> PRT

<213> Homo sapiens

<400> 28

Met	Glu	Lys	Glu	Leu	Arg	Ser	Thr	Ile	Leu	Phe	Asn	Ala	Tyr	Lys	Lys
1				5					10					15	
Glu	Ile	Phe	Thr	Thr	Asn	Asn	Gly	Tyr	Lys	Ser	Met	Gln	Lys	Lys	Leu
			20					25					30		
Arg	Ser	Asn	Trp	Lys	Ile	Gln	Ser	Leu	Lys	Asp	Glu	Ile	Thr	Ser	Glu
		35				40						45			
Lys	Leu	Asn	Gly	Val	Lys	Leu	Trp	Ile	Thr	Ala	Gly	Pro	Arg	Glu	Lys
	50					55					60				
Phe	Thr	Ala	Ala	Glu	Phe	Glu	Ile	Leu	Lys	Lys	Tyr	Leu	Asp	Thr	Gly
65					70					75					80
Gly	Asp	Val	Leu	Val	Met	Leu	Gly	Glu	Gly	Gly	Glu	Ser	Arg	Phe	Asp
				85					90					95	
Thr	Asn	Ile	Asn	Phe	Leu	Leu	Glu	Glu	Tyr	Gly	Ile	Met	Val	Asn	Asn
			100					105					110		
Asp	Ala	Val	Val	Arg	Asn	Val	Tyr	His	Lys	Tyr	Phe	His	Pro	Lys	Glu
		115					120					125			
Ala	Leu	Val	Ser	Ser	Gly	Val	Leu	Asn	Arg	Glu	Ile	Ser	Arg	Ala	Ala
	130					135					140				
Gly	Lys	Ala	Val	Leu	Ala	Ile	Ile	Asp	Glu	Glu	Ser	Ser	Gly	Asn	Asn
145					150					155					160
Ala	Gln	Ala	Leu	Thr	Phe	Val	Tyr	Pro	Phe	Gly	Ala	Thr	Leu	Ser	Val
				165					170					175	
Met	Lys	Pro	Ala	Val	Ala	Val	Leu	Ser	Thr	Gly	Ser	Val	Cys	Phe	Pro
		180						185					190		
Leu	Asn	Arg	Pro	Ile	Leu	Ala	Phe	Tyr	His	Ser	Lys	Asn	Gln	Gly	Gly
	195						200					205			
Lys	Leu	Ala	Val	Leu	Gly	Ser	Cys	His	Met	Phe	Ser	Asp	Gln	Tyr	Leu
	210					215					220				
Asp	Lys	Glu	Glu	Asn	Ser	Lys	Ile	Met	Asp	Val	Val	Val	Phe	Gln	Trp
225				230						235					240
Leu	Thr	Thr	Gly	Asp	Ile	His	Leu	Asn	Gln	Ile	Asp	Ala	Glu	Asp	Pro
			245						250					255	
Glu	Ile	Ser	Asp	Tyr	Met	Met	Leu	Pro	Tyr	Thr	Ala	Thr	Leu	Ser	Lys
		260						265					270		
Arg	Asn	Arg	Glu	Cys	Leu	Gln	Glu	Ser	Asp	Glu	Ile	Pro	Arg	Asp	Phe
	275						280					285			
Thr	Thr	Leu	Phe	Asp	Leu	Ser	Ile	Phe	Gln	Leu	Asp	Thr	Thr	Ser	Phe
	290					295					300				
His	Ser	Val	Ile	Glu	Ala	His	Glu	Gln	Leu	Asn	Val	Lys	His	Glu	Pro
305					310					315					320

Leu Gln Leu Ile Gln Pro Gln Phe Glu Thr Pro Leu Pro Thr Leu Gln
 325 330 335
 Pro Ala Val Phe Pro Pro Ser Phe Arg Glu Leu Pro Pro Pro Pro Leu
 340 345 350
 Glu Leu Phe Asp Leu Asp Glu Thr Phe Ser Ser Glu Lys Ala Arg Leu
 355 360 365
 Ala Gln Ile Thr Asn Lys Cys Thr Glu Glu Asp Leu Glu Phe Tyr Val
 370 375 380
 Arg Lys Cys Gly Asp Ile Leu Gly Val Thr Ser Lys Leu Pro Lys Asp
 385 390 395 400
 Gln Gln Asp Ala Lys His Ile Leu Glu His Val Phe Phe Gln Val Val
 405 410 415
 Glu Phe Lys Lys Leu Asn Gln Glu His Asp Ile Asp Thr Ser Glu Thr
 420 425 430
 Ala Phe Gln Asn Asn Phe
 435

<210> 29

<211> 472

<212> PRT

<213> Caenorhabditis elegans

<400> 29

Met Pro Pro Phe Ser Asp Glu Lys Met Thr Asn Arg Ser Ile Gly Arg
 1 5 10 15
 Lys Val Leu Ile Asp Gln Ser Lys Gln Gln Ile Ser Leu Ile Ser
 20 25 30
 Gly Phe Arg Gly Val Ala Arg His Leu Lys Ser Val Leu Thr Val Glu
 35 40 45
 Ile Asn Thr Glu Pro Ile Asn Leu Asn Gly Leu Glu Asp Val Arg Met
 50 55 60
 Leu Ile Ile Pro Gln Pro Lys Thr Ser Phe Gly Thr Gly Glu Ile Glu
 65 70 75 80
 Ala Ile Trp Lys Phe Val Glu Glu Gly Gly Ser Leu Met Ile Leu Ser
 85 90 95
 Gly Glu Gly Gly Glu Arg Gln Ser Leu Asn Glu Met Ile Ala Lys Tyr
 100 105 110
 Gly Ile Thr Val Asn Lys Asp Ser Val Ile Arg Thr Val Phe Leu Lys
 115 120 125
 Tyr Phe Asp Pro Lys Glu Ala Leu Val Ala Asn Gly Val Ile Asn Arg
 130 135 140
 Ala Ile Ala Val Ala Ala Lys Lys Asn Val Ser Thr Glu Gln Lys His
 145 150 155 160
 Asn Ser Gln Ala Leu Ser Phe Ile Tyr Pro Tyr Gly Cys Thr Leu Asp
 165 170 175
 Val Asn Asn Arg Met Ser Asn Val Val Leu Ser Ser Gly Ser Thr Ser
 180 185 190
 Phe Pro Thr Ser Arg Pro Val Ala Ala Phe His Glu Thr Lys Leu Asn
 195 200 205
 Glu Met Lys Lys Lys Gly Arg Val Cys Val Val Gly Ser Val Ser Met
 210 215 220
 Phe His Asp Thr Tyr Ile Asp Lys Glu Glu Asn Gly Lys Ile Phe Asp
 225 230 235 240
 Thr Phe Val Glu Phe Leu Val Asn Gly Leu Glu Leu Asn Thr Ile Asp
 245 250 255
 Ala Ala Glu Pro Glu Ile Asn Asp Tyr Thr Asn Ile Pro Asp His Ile
 260 265 270

His	Met	Ser	Gln	Gln	Ile	Lys	Val	Cys	Met	Tyr	Glu	Gly	Glu	Leu	Asp
	275						280					285			
Gln	Ala	Ile	Ser	Ser	Asp	Phe	Met	Lys	Ile	Met	Asp	Thr	Ser	Leu	His
	290					295					300				
Ser	Phe	Asn	Leu	Lys	His	Trp	Pro	Met	Thr	Ile	Arg	Leu	Tyr	Glu	Ala
305				310					315						320
Leu	Asn	Leu	Ser	Pro	Pro	Leu	Thr	Leu	Val	Glu	Pro	Gln	Phe	Glu	
			325					330					335		
Leu	Pro	Met	Pro	Pro	Phe	Gln	Pro	Ala	Val	Phe	Pro	Pro	Thr	Phe	Gln
		340					345						350		
Glu	Leu	Pro	Met	Pro	Pro	Leu	Glu	Phe	Asp	Leu	Asp	Glu	Gln	Phe	
	355					360					365				
Ser	Ser	Pro	Glu	Ile	Gln	Leu	Ser	Gln	Leu	Ala	Asn	Arg	Ser	Glu	Glu
	370					375					380				
Glu	Asp	Leu	Ile	Phe	Phe	Ile	Glu	Lys	Ala	Gly	Glu	Ile	Thr	Gly	Ile
385				390					395						400
Ser	Ala	Glu	Leu	Thr	Arg	Ser	Glu	Arg	Thr	Pro	Lys	Lys	Ile	Ile	Glu
			405				410						415		
Leu	Ala	Val	Ser	Lys	Leu	Met	Leu	Phe	Lys	Arg	Ser	Met	Met	Asp	Gly
		420					425					430			
Glu	Leu	Glu	Val	Ala	Ser	Ala	Phe	Asp	Ile	Gly	Glu	His	Asp	Ala	His
	435					440					445				
His	Gln	Ser	Phe	Asn	Gln	Gly	Glu	Glu	Met	Asp	Glu	Gln	Leu	Phe	Ser
	450				455						460				
Asp	Ile	Asp	Glu	Phe	Asp	Asp	Leu								
465				470											

<210> 30

<211> 429

<212> PRT

<213> Homo sapiens

<400> 30

Met	Thr	Ala	Ala	Leu	Ala	Val	Val	Thr	Thr	Ser	Gly	Leu	Glu	Asp	Gly
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Val	Pro	Arg	Ser	Arg	Gly	Glu	Gly	Thr	Gly	Glu	Val	Val	Leu	Glu	Arg
		20					25						30		
Gly	Pro	Gly	Ala	Ala	Tyr	His	Met	Phe	Val	Val	Met	Glu	Asp	Leu	Val
	35					40					45				
Glu	Lys	Leu	Lys	Leu	Leu	Arg	Tyr	Glu	Glu	Glu	Phe	Leu	Arg	Lys	Ser
	50				55					60					
Asn	Leu	Lys	Ala	Pro	Ser	Arg	His	Tyr	Phe	Ala	Leu	Pro	Thr	Asn	Pro
65				70					75					80	
Gly	Glu	Gln	Phe	Tyr	Met	Phe	Cys	Thr	Leu	Ala	Ala	Trp	Leu	Ile	Asn
		85						90					95		
Lys	Ala	Gly	Arg	Pro	Phe	Glu	Gln	Pro	Gln	Glu	Tyr	Asp	Asp	Pro	Asn
		100					105					110			
Ala	Thr	Ile	Ser	Asn	Ile	Leu	Ser	Glu	Leu	Arg	Ser	Phe	Gly	Arg	Thr
	115					120						125			
Ala	Asp	Phe	Pro	Pro	Ser	Lys	Leu	Lys	Ser	Gly	Tyr	Gly	Glu	His	Val
	130				135					140					
Cys	Tyr	Val	Leu	Asp	Cys	Phe	Ala	Glu	Glu	Ala	Leu	Lys	Tyr	Ile	Gly
145				150					155					160	
Phe	Thr	Trp	Lys	Arg	Pro	Ile	Tyr	Pro	Val	Glu	Glu	Leu	Glu	Glu	Glu
		165					170						175		
Ser	Val	Ala	Glu	Asp	Asp	Ala	Glu	Leu	Thr	Leu	Asn	Lys	Val	Asp	Glu
		180					185						190		

Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu
 195 200 205
 Asn Val Leu Lys Ala Gln Thr Tyr His Leu Asp Met Asn Glu Thr Ala
 210 215 220
 Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser
 225 230 235 240
 Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr
 245 250 255
 Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Arg
 260 265 270
 Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys
 275 280 285
 Leu His Asn Glu Ile Thr Arg Thr Leu Glu Lys Ile Ser Ser Arg Glu
 290 295 300
 Lys Tyr Ile Asn Asn Gln Leu Glu Asn Leu Val Gln Glu Tyr Arg Ala
 305 310 315 320
 Ala Gln Ala Gln Leu Ser Glu Ala Lys Glu Arg Tyr Gln Gln Gly Asn
 325 330 335
 Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Met Glu Glu
 340 345 350
 Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr
 355 360 365
 Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys
 370 375 380
 Gln Glu Thr Val Glu Met Asp Ile Arg Ile Gly Ile Val Glu His Thr
 385 390 395 400
 Leu Leu Gln Ser Lys Leu Lys Glu Lys Ser Asn Met Thr Arg Asn Met
 405 410 415
 His Ala Thr Val Ile Pro Glu Pro Ala Thr Gly Phe Tyr
 420 425

<210> 31
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 31
 Asp Gln Arg Ile His Val Asp Gln Met Tyr Gln His Lys Ser Gly Ile
 1 5 10 15
 Glu Ser Ser Leu Lys Glu Ser Lys Arg Phe Phe Asp Lys Leu His Asn
 20 25 30
 Glu Ile Ser Lys Thr Leu Glu Lys Ile Ser His Cys Glu Lys Tyr Ile
 35 40 45
 Asn His Gln Leu Glu His Arg Val Gln Glu Tyr Pro Ala Ala Gln Thr
 50 55 60
 Gln Leu Ser Asp Val Arg Ser Gln Gln Gly Ser Gly Gly Val Ile Glu
 65 70 75 80
 Arg Thr Arg Leu Leu Ser Glu Ala Thr Glu Asp Thr Glu His Val Lys
 85 90 95
 Leu Glu Met Glu Glu Lys Cys Ser Ser Met Thr Asp Gly Asp Ser Leu
 100 105 110
 Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys Gln Glu Thr Val Gln
 115 120 125
 Met Asp Ile Arg Ile Gly Val Val Glu His Thr Leu Leu
 130 135 140

<210> 32
 <211> 325
 <212> PRT
 <213> *Caenorhabditis elegans*

<400> 32
 Met Leu His His Ile Lys Ser Leu Lys Ser Val Leu Ser Arg Gly Gln
 1 5 10 15
 Glu Gly Arg Phe Gly Glu Lys Arg His Ser Asn Thr Thr Phe Ile Thr
 20 25 30
 Gly Ile Ala Thr Asp Phe Thr Ala Ala Lys Leu Lys Ser Gly Ala Gly
 35 40 45
 Glu Asn Val Ile Phe Ile Leu Asn Ser Leu Ala Asp Ala Ser Leu Val
 50 55 60
 His Val Gly Phe Gln Trp Gln Lys Met Ile Pro Pro Lys Glu Glu Asp
 65 70 75 80
 Glu Asp Thr Ala Val Asp Glu Gln Asp Glu Asp Asp Asp Asn Asp Asp
 85 90 95
 Ile Val Glu Glu Pro Met Asn Phe Leu Asp Asp Asp Asp Asp Asp Asn
 100 105 110
 Val Ile Glu Ile Asp Leu Lys Ala Gln Gly Leu Ala Thr Glu Ser Lys
 115 120 125
 Asn Pro Leu Gln Ser Val Leu Gln Ser Asn Thr Asp Ala Ile Thr Trp
 130 135 140
 Lys Gln Glu Val Glu Arg Val Ala Pro Gln Leu Lys Ile Thr Leu Lys
 145 150 155 160
 Gln Asp Ala Lys Asp Trp Arg Leu His Leu Glu Gln Met Asn Ser Met
 165 170 175
 His Lys Asn Val Glu Gln Lys Val Gly Asn Val Gly Pro Tyr Leu Asp
 180 185 190
 Asn Met Ser Lys Asp Ile Ala Lys Ala Leu Glu Arg Ile Ala Ser Arg
 195 200 205
 Glu Lys Ser Leu Asn Ser Gln Leu Ala Ser Met Met Ser Lys Phe Arg
 210 215 220
 Arg Ala Thr Asp Thr Arg Ala Glu Leu Arg Glu Lys Tyr Lys Ala Ala
 225 230 235 240
 Ser Val Gly Val Ser Ser Arg Thr Glu Thr Leu Asp Arg Ile Ser Asp
 245 250 255
 Asp Ile Glu Gln Leu Lys Gln Gln Ile Glu Glu Gln Gly Ala Lys Ser
 260 265 270
 Ser Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ala Val Ser Lys Leu
 275 280 285
 Glu Glu Glu Leu Gln Thr Met Asn Val Gln Ile Gly Val Phe Glu Gln
 290 295 300
 Ser Ile Leu Asn Thr Tyr Leu Arg Asp His Phe Asn Phe Ser Ala Asn
 305 310 315 320
 Leu Leu Asn Ile Met
 325

<210> 33
 <211> 435
 <212> PRT
 <213> *Homo sapiens*

<400> 33
 Met Glu Glu Val Met Asn Gly Tyr Asn Met Leu Lys Ala Gln Asn Asp
 1 5 10 15

Arg	Glu	Thr	Gln	Ser	Leu	Asp	Val	Ile	Phe	Thr	Glu	Arg	Gln	Ala	Lys	
			20					25					30			
Glu	Lys	Gln	Ile	Arg	Ser	Val	Glu	Glu	Glu	Ile	Glu	Gln	Glu	Lys	Gln	
		35					40					45				
Ala	Thr	Asp	Asp	Ile	Ile	Lys	Asn	Met	Ser	Leu	Glu	Asn	Gln	Val	Lys	
		50				55					60					
Tyr	Leu	Glu	Met	Lys	Thr	Thr	Asn	Glu	Lys	Leu	Leu	Gln	Glu	Leu	Asp	
	65				70					75					80	
Thr	Leu	Gln	Gln	Gln	Leu	Asp	Ser	Gln	Asn	Met	Lys	Lys	Glu	Ser	Leu	
				85					90						95	
Glu	Ala	Glu	Ile	Ala	His	Ser	Gln	Val	Lys	Gln	Glu	Ala	Val	Leu	Leu	
			100					105					110			
His	Glu	Lys	Leu	Tyr	Glu	Leu	Glu	Ser	His	Arg	Asp	Gln	Met	Ile	Ala	
		115					120					125				
Glu	Asp	Lys	Ser	Ile	Gly	Ser	Pro	Met	Glu	Glu	Arg	Glu	Lys	Leu	Leu	
	130					135					140					
Lys	Gln	Ile	Lys	Asp	Asp	Asn	Gln	Glu	Ile	Ala	Ser	Met	Glu	Arg	Gln	
	145				150					155					160	
Leu	Thr	Asp	Thr	Lys	Glu	Lys	Ile	Asn	Gln	Phe	Ile	Glu	Glu	Ile	Arg	
			165						170						175	
Gln	Leu	Asp	Met	Asp	Leu	Glu	Glu	His	Gln	Gly	Glu	Met	Asn	Gln	Lys	
			180					185					190			
Tyr	Lys	Glu	Leu	Lys	Lys	Arg	Glu	Glu	His	Met	Asp	Thr	Phe	Ile	Glu	
	195						200					205				
Thr	Phe	Glu	Glu	Thr	Lys	Asn	Gln	Glu	Leu	Lys	Arg	Lys	Ala	Gln	Ile	
	210					215						220				
Glu	Ala	Asn	Ile	Val	Ala	Leu	Leu	Glu	His	Cys	Ser	Arg	Asn	Ile	Asn	
	225				230					235					240	
Arg	Ile	Glu	Gln	Ile	Ser	Ser	Ile	Thr	Asn	Gln	Glu	Leu	Lys	Met	Met	
			245						250					255		
Gln	Asp	Asp	Leu	Asn	Phe	Lys	Ser	Thr	Glu	Val	Gln	Lys	Ser	Gln	Ser	
			260					265					270			
Thr	Ala	Gln	Asn	Leu	Thr	Ser	Asp	Ile	Gln	Arg	Leu	Gln	Leu	Asp	Leu	
		275					280						285			
Gln	Lys	Met	Glu	Leu	Leu	Glu	Ser	Lys	Met	Thr	Glu	Glu	Gln	His	Ser	
	290					295					300					
Leu	Lys	Ser	Lys	Ile	Lys	Gln	Met	Thr	Thr	Asp	Leu	Glu	Ile	Tyr	Asn	
	305				310					315					320	
Asp	Leu	Pro	Ala	Leu	Lys	Ser	Ser	Gly	Glu	Glu	Lys	Ile	Lys	Lys	Leu	
			325					330						335		
His	Gln	Glu	Arg	Met	Ile	Leu	Ser	Thr	His	Arg	Asn	Ala	Phe	Lys	Lys	
			340					345					350			
Ile	Met	Glu	Lys	Gln	Asn	Ile	Glu	Tyr	Glu	Ala	Leu	Lys	Thr	Gln	Leu	
		355					360						365			
Gln	Glu	Asn	Glu	Thr	His	Ser	Gln	Leu	Thr	Asn	Leu	Glu	Arg	Lys	Trp	
	370					375					380					
Gln	His	Leu	Glu	Gln	Asn	Asn	Phe	Ala	Met	Lys	Glu	Phe	Ile	Ala	Thr	
	385				390					395					400	
Lys	Ser	Gln	Glu	Ser	Asp	Tyr	Gln	Pro	Ile	Lys	Lys	Asn	Val	Thr	Lys	
			405					410					415			
Gln	Ile	Ala	Glu	Tyr	Asn	Lys	Thr	Ile	Val	Asp	Ala	Leu	His	Ser	Thr	
			420					425					430			
Ser	Gly	Asn														
		435														

<210> 34

<211> 824

<212> PRT

<213> Homo sapiens

<400> 34

Met	Met	Gln	Asn	Val	His	Leu	Ala	Pro	Glu	Thr	Asp	Glu	Asp	Asp	Leu	1	5	10	15
Tyr	Ser	Gly	Tyr	Asn	Asp	Tyr	Asn	Pro	Ile	Tyr	Asp	Ile	Glu	Glu	Leu	20	25	30	
Glu	Asn	Asp	Ala	Ala	Phe	Gln	Gln	Ala	Val	Arg	Thr	Ser	His	Gly	Arg	35	40	45	
Arg	Pro	Pro	Ile	Thr	Ala	Lys	Ile	Ser	Ser	Thr	Ala	Val	Thr	Arg	Pro	50	55	60	
Ile	Ala	Thr	Gly	Tyr	Gly	Ser	Lys	Thr	Ser	Leu	Ala	Ser	Ser	Ile	Gly	65	70	75	80
Arg	Pro	Met	Thr	Gly	Ala	Ile	Gln	Asp	Gly	Val	Thr	Arg	Pro	Met	Thr	85	90	95	
Ala	Val	Arg	Ala	Ala	Gly	Phe	Thr	Lys	Ala	Ala	Leu	Arg	Gly	Ser	Ala	100	105	110	
Phe	Asp	Pro	Leu	Ser	Gln	Ser	Arg	Gly	Pro	Ala	Ser	Pro	Leu	Glu	Ala	115	120	125	
Lys	Lys	Lys	Asp	Ser	Pro	Glu	Glu	Lys	Ile	Lys	Gln	Leu	Glu	Lys	Glu	130	135	140	
Val	Asn	Glu	Leu	Val	Glu	Glu	Ser	Cys	Ile	Ala	Asn	Ser	Cys	Gly	Asp	145	150	155	160
Leu	Lys	Leu	Ala	Leu	Glu	Lys	Ala	Lys	Asp	Ala	Gly	Arg	Lys	Glu	Arg	165	170	175	
Val	Leu	Val	Arg	Gln	Arg	Glu	Gln	Val	Thr	Thr	Pro	Glu	Asn	Ile	Asn	180	185	190	
Leu	Asp	Leu	Thr	Tyr	Ser	Val	Leu	Ser	Asn	Leu	Ala	Ser	Gln	Tyr	Ser	195	200	205	
Val	Asn	Glu	Met	Tyr	Ala	Glu	Ala	Leu	Asn	Thr	Tyr	Gln	Val	Ile	Val	210	215	220	
Lys	Asn	Lys	Met	Phe	Ser	Asn	Ala	Gly	Ile	Leu	Lys	Met	Asn	Met	Gly	225	230	235	240
Asn	Ile	Tyr	Leu	Lys	Gln	Arg	Asn	Tyr	Ser	Lys	Ala	Ile	Lys	Phe	Tyr	245	250	255	
Arg	Met	Ala	Leu	Asp	Gln	Val	Pro	Ser	Val	Asn	Lys	Gln	Met	Arg	Ile	260	265	270	
Lys	Ile	Met	Gln	Asn	Ile	Gly	Val	Thr	Phe	Ile	Gln	Ala	Gly	Gln	Tyr	275	280	285	
Ser	Asp	Ala	Ile	Asn	Ser	Tyr	Glu	His	Ile	Met	Ser	Met	Ala	Pro	Asn	290	295	300	
Leu	Lys	Ala	Gly	Tyr	Asn	Leu	Thr	Ile	Cys	Tyr	Phe	Ala	Ile	Gly	Asp	305	310	315	320
Arg	Glu	Lys	Met	Lys	Lys	Ala	Phe	Gln	Lys	Leu	Ile	Thr	Val	Pro	Leu	325	330	335	
Glu	Ile	Asp	Glu	Asp	Lys	Tyr	Ile	Ser	Pro	Ser	Asp	Asp	Pro	His	Thr	340	345	350	
Asn	Leu	Val	Thr	Glu	Ala	Ile	Lys	Asn	Asp	His	Leu	Arg	Gln	Met	Glu	355	360	365	
Arg	Glu	Arg	Lys	Ala	Met	Ala	Glu	Lys	Tyr	Ile	Thr	Thr	Ser	Ala	Lys	370	375	380	
Leu	Ile	Ala	Pro	Val	Ile	Glu	Thr	Ser	Phe	Ala	Ala	Gly	Cys	Asp	Trp	385	390	395	400
Cys	Val	Glu	Val	Val	Lys	Ala	Ser	Gln	Tyr	Val	Glu	Leu	Ala	Asn	Asp	405	410	415	

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Leu Glu Ile Asn Lys Ala Val Thr Tyr Leu Arg Gln Lys Asp Tyr Asn
      420                      425                      430
Gln Ala Val Glu Ile Leu Lys Val Leu Glu Lys Lys Asp Asn Arg Val
      435                      440                      445
Lys Ser Ala Ala Ala Thr Asn Leu Ser Ala Leu Tyr Tyr Met Gly Lys
      450                      455                      460
Asp Phe Ala Gln Ala Ser Ser Tyr Ala Asp Ile Ala Val Asn Ser Asp
      465                      470                      475                      480
Arg Tyr Asn Pro Ala Ala Leu Thr Asn Lys Gly Asn Thr Val Phe Ala
      485                      490                      495
Asn Gly Asp Tyr Glu Lys Ala Ala Glu Phe Tyr Lys Glu Ala Leu Arg
      500                      505                      510
Asn Asp Ser Ser Cys Thr Glu Ala Leu Tyr Asn Ile Gly Leu Thr Tyr
      515                      520                      525
Glu Lys Leu Asn Arg Leu Asp Glu Ala Leu Asp Cys Phe Leu Lys Leu
      530                      535                      540
His Ala Ile Leu Arg Asn Ser Ala Glu Val Leu Tyr Gln Ile Ala Asn
      545                      550                      555                      560
Ile Tyr Glu Leu Met Glu Asn Pro Ser Gln Ala Ile Glu Trp Leu Met
      565                      570                      575
Gln Val Val Ser Val Ile Pro Thr Asp Pro Gln Val Leu Ser Lys Leu
      580                      585                      590
Gly Glu Leu Tyr Asp Arg Glu Gly Asp Lys Ser Gln Ala Phe Gln Tyr
      595                      600                      605
Tyr Tyr Glu Ser Tyr Arg Tyr Phe Pro Cys Asn Ile Glu Val Ile Glu
      610                      615                      620
Trp Leu Gly Ala Tyr Tyr Ile Asp Thr Gln Phe Trp Glu Lys Ala Ile
      625                      630                      635                      640
Gln Tyr Phe Glu Arg Ala Ser Leu Ile Gln Pro Thr Gln Val Lys Trp
      645                      650                      655
Gln Leu Met Val Ala Ser Cys Phe Arg Arg Ser Gly Asn Tyr Gln Lys
      660                      665                      670
Ala Leu Asp Thr Tyr Lys Asp Thr His Arg Lys Phe Pro Glu Asn Val
      675                      680                      685
Glu Cys Leu Arg Phe Leu Val Arg Leu Cys Thr Asp Leu Gly Leu Lys
      690                      695                      700
Asp Ala Gln Glu Tyr Ala Arg Lys Leu Lys Arg Leu Glu Lys Met Lys
      705                      710                      715                      720
Glu Ile Arg Glu Gln Arg Ile Lys Ser Gly Arg Asp Gly Ser Gly Gly
      725                      730                      735
Ser Arg Gly Lys Arg Glu Gly Ser Ala Ser Gly Asp Ser Gly Gln Asn
      740                      745                      750
Tyr Ser Ala Ser Ser Lys Gly Glu Arg Leu Ser Ala Arg Leu Arg Ala
      755                      760                      765
Leu Pro Gly Thr Asn Glu Pro Tyr Glu Ser Ser Ser Asn Lys Glu Ile
      770                      775                      780
Asp Ala Ser Tyr Val Asp Pro Leu Gly Pro Gln Ile Glu Arg Pro Lys
      785                      790                      795                      800
Thr Ala Ala Lys Lys Arg Ile Asp Glu Asp Asp Phe Ala Asp Glu Glu
      805                      810                      815
Leu Gly Asp Asp Leu Leu Pro Glu
      820

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<210> 35

<211> 820

<212> PRT

<213> Caenorhabditis elegans

<400> 35

Met	Ala	Asn	Ser	Thr	Phe	Arg	Glu	Asp	Asp	Asp	Asp	Phe	Tyr	Gly	Gly
1				5				10						15	
Phe	Asp	Ser	Tyr	Asp	Lys	Ala	Tyr	Asp	Ile	Gln	Asn	Ile	Thr	Gln	Asn
		20						25					30		
Pro	Gln	Phe	Gln	Gln	Ala	Val	Ala	Arg	Ser	Ser	His	Gly	Arg	Arg	Pro
		35					40					45			
Thr	Ala	Ser	Gln	Met	Gly	Phe	Arg	Asp	Ala	Ser	Ser	Ser	Tyr	Gly	Lys
	50					55					60				
Pro	Pro	Gly	Thr	Met	Met	Gly	Asn	Gln	Ser	Arg	Met	Gly	Gly	Arg	Thr
65				70						75					80
Ala	Met	Ala	Asn	Asn	Asn	Glu	Pro	Ala	Arg	Pro	Met	Thr	Ala	Val	Arg
				85					90					95	
Gly	Ala	Gly	Tyr	Thr	Ser	Phe	Ala	Asn	Lys	Val	Gln	Ala	Ala	Glu	Arg
			100					105					110		
Pro	Leu	Ser	Thr	Glu	Asn	Ser	Gly	Glu	Asn	Gly	Glu	Glu	Lys	Cys	Arg
		115					120					125			
Gln	Met	Glu	Asn	Lys	Val	Met	Glu	Met	Leu	Arg	Glu	Ser	Met	Leu	Ala
	130					135					140				
Ser	Glu	Lys	Lys	Lys	Phe	Lys	Glu	Ala	Leu	Asp	Lys	Ala	Lys	Glu	Ala
145					150					155					160
Gly	Arg	Arg	Glu	Arg	Ala	Val	Val	Lys	His	Arg	Glu	Gln	Gln	Gly	Leu
				165					170					175	
Val	Glu	Met	Met	Asn	Leu	Asp	Leu	Thr	Phe	Thr	Val	Leu	Phe	Asn	Leu
			180				185						190		
Ala	Gln	Gln	Tyr	Glu	Ala	Asn	Asp	Met	Thr	Asn	Glu	Ala	Leu	Asn	Thr
			195				200					205			
Tyr	Glu	Ile	Ile	Val	Arg	Asn	Lys	Met	Phe	Pro	Asn	Ser	Gly	Arg	Leu
	210					215					220				
Lys	Val	Asn	Ile	Gly	Asn	Ile	His	Phe	Arg	Lys	Arg	Glu	Phe	Thr	Lys
225					230					235					240
Ala	Leu	Lys	Tyr	Tyr	Arg	Met	Ala	Leu	Asp	Gln	Val	Pro	Ser	Ile	Gln
				245					250					255	
Lys	Asp	Thr	Arg	Ile	Lys	Ile	Leu	Asn	Asn	Ile	Gly	Val	Thr	Phe	Val
			260				265						270		
Arg	Met	Gly	Ser	Tyr	Asp	Asp	Ala	Ile	Ser	Thr	Phe	Asp	His	Cys	Val
		275					280					285			
Glu	Glu	Asn	Pro	Asn	Phe	Ile	Thr	Ala	Leu	Asn	Leu	Ile	Leu	Val	Ala
	290					295					300				
Phe	Cys	Ile	Gln	Asp	Ala	Glu	Lys	Met	Arg	Glu	Ala	Phe	Val	Lys	Met
305				310						315					320
Ile	Asp	Ile	Pro	Gly	Phe	Pro	Asp	Asp	Asp	Tyr	Met	Lys	Glu	Lys	Asp
				325					330					335	
Asp	Asp	Asp	Val	Leu	Leu	Asn	Gln	Thr	Leu	Asn	Ser	Asp	Met	Leu	Lys
			340					345					350		
Asn	Trp	Glu	Lys	Arg	Asn	Lys	Ser	Asp	Ala	Glu	Lys	Ala	Ile	Ile	Thr
		355					360						365		
Ala	Val	Lys	Ile	Ile	Ser	Pro	Val	Ile	Ala	Pro	Asp	Tyr	Ala	Ile	Gly
	370					375					380				
Tyr	Glu	Trp	Cys	Leu	Glu	Ser	Leu	Lys	Gln	Ser	Val	His	Ala	Pro	Leu
385					390					395					400
Ala	Ile	Glu	Leu	Glu	Met	Thr	Lys	Ala	Gly	Glu	Leu	Met	Lys	Asn	Gly
				405					410					415	
Asp	Ile	Glu	Gly	Ala	Ile	Glu	Val	Leu	Lys	Val	Phe	Asn	Ser	Gln	Asp
			420					425					430		

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<210> 36
<211> 1198
<212> PRT
<213> Homo sapiens
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<213> Homo sapiens

<400> 36

Thr	Leu	Leu	Gln	Pro	Leu	Lys	Gly	His	Lys	Asp	Thr	Val	Tyr	Cys	Val
1				5					10					15	
Ala	Tyr	Ala	Lys	Asp	Gly	Lys	Arg	Phe	Ala	Ser	Gly	Ser	Ala	Asp	Lys
			20					25					30		
Ser	Val	Ile	Ile	Trp	Thr	Ser	Lys	Leu	Glu	Gly	Ile	Leu	Lys	Tyr	Thr
		35					40					45			
His	Asn	Asp	Ala	Ile	Gln	Cys	Val	Ser	Tyr	Asn	Pro	Ile	Thr	His	Gln
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Gln	Lys	Leu	Gln	Gly	Phe	Val	Val	Gly	Tyr	Asn	Gly	Ser	Lys	Ile	Phe
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Cys	Leu	His	Val	Phe	Ser	Ile	Ser	Ala	Val	Glu	Val	Pro	Gln	Ser	Ala
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Glu	Ser	Arg	Phe	Asn	Asp	Ala	Ala	Tyr	Tyr	Tyr	Trp	Met	Leu	Ser	Met
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Gln	Cys	Leu	Asp	Ile	Ala	Gln	Asp	Pro	Ala	Gln	Lys	Asp	Thr	Met	Leu
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Gly Lys Phe Tyr His Phe Gln Arg Leu Ala Glu Leu Tyr His Gly Tyr
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 His Ala Ile His Arg His Thr Glu Asp Pro Phe Ser Val His Arg Pro
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 Glu Thr Leu Phe Asn Ile Ser Arg Phe Leu Leu His Ser Leu Pro Lys
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 35 40 45
 Gln Met Gln Thr Leu Lys Gly His Lys Asp Leu Val Tyr Thr Val Ala
 50 55 60
 Trp Ser His Asn Gly Glu Leu Phe Ala Ser Gly Gly Ala Asp Lys Leu
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 Val Ile Leu Trp Asn Glu Lys His Glu Gly Thr Leu Arg Tyr Ser His
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Gln	Arg	Asp	Asn	Glu	Pro	Ile	Trp	Gly	Ile	Ala	Phe	Ser	Ser	Asn	Arg
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Lys	Ile	Leu	Lys	Ile	Tyr	Thr	Arg	Lys	Gly	Val	Leu	Leu	Gly	Thr	Val
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465					470					475					480
Asp	Ile	Asn	Ala	Asn	Arg	Thr	Val	Leu	Ala	Ser	Ile	Glu	Asp	Thr	Leu
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Arg	Thr	Phe	Cys	Leu	Val	Gln	Tyr	Asn	Leu	Ile	Pro	Leu	Glu	Val	Pro
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Tyr	Thr	Ile	His	Leu	Tyr	Gln	Tyr	Ile	Glu	Arg	Gly	Asp	Phe	Lys	Glu
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Thr	Lys	Lys	Met	Leu	Met	Arg	Lys	Arg	Ala	Ser	Trp	Ala	Arg	Asp	Ala
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Asn	Gln	Pro	Lys	Ile	Ala	Ala	Glu	Met	Leu	Ile	Ser	Ser	Gly	Asp	Leu
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Asp	Lys	Ala	Ala	Leu	Leu	Ile	Ile	Asp	Asn	Asp	Trp	Leu	Glu	Leu	Ala
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Ile	Glu	Ile	Ser	His	Lys	Ile	Asp	Arg	Ser	Asp	Leu	Glu	Thr	Met	Lys
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Val	Asn	Ala	Gly	His	Trp	Thr	Asp	Ala	Phe	Ala	Ile	Ala	Asp	Arg	His
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Pro	Lys	Tyr	Val	Glu	Asp	Val	Tyr	Leu	Pro	Tyr	Ala	Arg	Phe	Leu	Ala
			820					825					830		
Glu	Arg	Asp	Arg	Phe	Glu	Glu	Ala	Gln	Lys	Ala	Phe	His	Arg	Ala	Gly
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Lys	Glu	Gln	Glu	Ala	Met	His	Val	Leu	Glu	Gln	Leu	Thr	Ser	Asn	Ser
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Val	Asn	Glu	Asn	Arg	Phe	Ala	Asp	Ala	Gly	Cys	Gly	Leu	Asn	Asn	Pro
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Leu	Leu	Gly	Gly	Met	Ser	Cys	Ile	His	Cys	Glu	Thr	Pro	Phe	Ile	Ile
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Ser	Phe	Val	Ser	Phe	Asp	Ile	Leu	Pro	Leu	Ile	Glu	Phe	Lys	Ile	Glu
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Gly	His	Val	Ile	Ile	Gln	Thr	Phe	Pro	Pro	Pro	Leu	Ala	Pro	Lys	Phe
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Pro	Val	Leu 35	Lys	Phe	Phe	Lys	Ala 40	Tyr	Gly	Val	Leu	Lys 45	Glu	Asp	Arg
Glu	Ala 50	Ile	Gln	Glu	Leu	Glu 55	Tyr	Ser	Leu	Lys	Glu 60	Ile	Arg	Lys	Thr
Val 65	Ser	Gly	Thr	Ala	Leu 70	Tyr	Tyr	Ala	Gly	Leu 75	Phe	Leu	Trp	Leu	Ile 80
Gly	Arg	His	Asp 85	Lys	Ala	Lys	Glu	Tyr	Ile 90	Asp	Arg	Met	Leu	Lys 95	Ile
Ser	Arg	Gly	Phe 100	Arg	Glu	Ala	Tyr	Val 105	Leu	Arg	Gly	Trp	Val 110	Asp	Leu
Thr	Ser	Asp 115	Lys	Pro	His	Thr	Ala 120	Lys	Lys	Ala	Ile	Glu 125	Tyr	Leu	Glu
Gln	Gly 130	Ile	Gln	Asp	Thr	Lys 135	Asp	Val	Leu	Gly	Leu 140	Met	Gly	Lys	Ala
Met 145	Tyr	Phe	Met	Met	Gln 150	Gln	Asn	Tyr	Ser	Glu 155	Ala	Leu	Glu	Val	Val 160
Asn	Gln	Ile	Thr 165	Val	Thr	Ser	Gly	Ser	Phe 170	Leu	Pro	Ala	Leu	Val 175	Leu
Lys	Met	Gln 180	Leu	Phe	Leu	Ala	Arg	Gln 185	Asp	Trp	Glu	Gln	Thr 190	Val	Glu
Met	Gly 195	His	Arg	Arg	Ile	Leu	Glu 200	Lys	Asp	Glu	Ser	Asn 205	Ile	Asp	Ala
Cys	Gln 210	Ile	Leu	Thr	Val	His 215	Glu	Leu	Ala	Arg	Glu 220	Gly	Asn	Met	Thr
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Arg	Glu	Pro	Glu	Asn 245	Pro	Ser	Leu	His	Leu 250	Lys	Lys	Ile	Ile	Val 255	Val
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Ser	Phe 275	Ile	Glu	Arg	Thr	Phe	Met 280	Ala	Thr	Pro	Ser	Tyr 285	Val	His	Val
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Ala 305	Leu	Leu	Trp	Tyr	Ser 310	Glu	Ala	Met	Lys	Leu 315	Asp	Lys	Asp	Gly	Met 320
Ala	Gly	Leu	Thr	Gly 325	Ile	Ile	Leu	Cys	His 330	Ile	Leu	Glu	Gly	His 335	Leu

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Asp	Asp	Val	Leu	Cys	Cys	Pro	Pro	Thr	Pro	Thr	Phe	Gln	Cys	Lys	Val
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Leu	Met	Ala	Gln	Val	Arg	Tyr	Tyr	Ser	Gly	Glu	Leu	Glu	Asn	Ala	Gln
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Ser	Ile	Leu	Gln	Arg	Cys	Leu	Glu	Leu	Asp	Pro	Ala	Ser	Val	Asp	Ala
	530				535						540				
His	Leu	Leu	Met	Cys	Gln	Ile	Tyr	Leu	Ala	Gln	Gly	Asn	Phe	Gly	Met
545				550						555					560
Cys	Phe	His	Cys	Leu	Glu	Leu	Gly	Val	Ser	His	Asn	Phe	Gln	Val	Val
			565					570					575		
Arg	Asp	His	Pro	Leu	Tyr	His	Leu	Ile	Lys	Ala	Arg	Ala	Leu	Asn	Lys
		580					585						590		
Ala	Gly	Asp	Tyr	Pro	Glu	Ala	Ile	Lys	Thr	Leu	Lys	Met	Val	Ile	Lys
	595						600					605			
Leu	Pro	Ala	Leu	Lys	Lys	Glu	Glu	Gly	Arg	Lys	Phe	Leu	Arg	Pro	Ser
	610					615					620				
Val	Gln	Pro	Ser	Gln	Arg	Ala	Ser	Ile	Leu	Leu	Glu	Leu	Val	Glu	Ala
625				630						635					640
Leu	Arg	Leu	Asn	Gly	Glu	Leu	His	Glu	Ala	Thr	Lys	Val	Met	Gln	Asp
			645					650					655		
Thr	Ile	Asn	Glu	Phe	Gly	Gly	Thr	Pro	Glu	Glu	Asn	Arg	Ile	Thr	Ile
	660						665						670		
Ala	Asn	Val	Asp	Leu	Val	Leu	Ser	Lys	Gly	Asn	Val	Asp	Val	Ala	Leu
	675						680					685			
Asn	Met	Leu	Arg	Asn	Ile	Leu	Pro	Lys	Gln	Ser	Cys	Tyr	Met	Glu	Ala
	690				695						700				
Arg	Glu	Lys	Met	Ala	Asn	Ile	Tyr	Leu	Gln	Thr	Leu	Arg	Asp	Arg	Arg
705				710						715					720
Leu	Tyr	Ile	Arg	Cys	Tyr	Glu	Leu	Cys	Glu	His	Leu	Pro	Gly	Pro	His
			725					730					735		
Thr	Ser	Leu	Leu	Leu	Gly	Asp	Ala	Leu	Met	Ser	Ile	Leu	Glu	Val	Ser
		740					745						750		
Glu	Arg	Pro	His	Ser	Leu	Ala	Lys	Trp	Pro	Pro	Ser	Leu	Pro	Ser	Pro
	755						760					765			
Val	Gly	Glu	Lys	Arg	Lys	Thr	Gln	Arg	His	Phe	Pro	His	Gln	Pro	Glu
	770					775					780				

Lys	Ala	Leu	Glu	Val	Tyr	Asp	Glu	Ala	Tyr	Arg	Gln	Asn	Pro	His	Asp	785	790	795	800
Ala	Ser	Leu	Ala	Ser	Arg	Ile	Gly	His	Ala	Tyr	Val	Lys	Ala	His	Gln	805	810		815
Tyr	Thr	Lys	Ala	Ile	Glu	Tyr	Tyr	Glu	Ala	Ala	Gln	Lys	Ile	Asn	Gly	820	825		830
Gln	Asp	Phe	Leu	Cys	Cys	Asp	Leu	Gly	Lys	Leu	Leu	Leu	Lys	Leu	Lys	835	840		845
Lys	Val	Asn	Lys	Ala	Glu	Lys	Val	Leu	Lys	Gln	Ala	Leu	Glu	His	Asp	850	855		860
Ile	Gly	Val	Gln	Asp	Ile	Pro	Ser	Met	Met	Asn	Asp	Val	Lys	Cys	Leu	865	870		880
Leu	Leu	Leu	Ala	Lys	Val	Tyr	Lys	Ser	His	Lys	Lys	Glu	Ala	Val	Ile	885	890		895
Glu	Thr	Leu	Asn	Lys	Val	Ile	Asp	Arg	Trp	Thr	Gln	Ala	Leu	Ala	Leu	900	905		910
Asp	Leu	Gln	Ser	Arg	Ile	Leu	Lys	Arg	Val	Pro	Leu	Glu	Gln	Pro	Glu	915	920		925
Met	Ile	Pro	Ser	Gln	Lys	Gln	Leu	Ala	Ala	Ser	Ile	Cys	Ile	Gln	Phe	930	935		940
Ala	Glu	His	Tyr	Leu	Ala	Glu	Lys	Glu	Tyr	Asp	Lys	Ala	Val	Gln	Ser	945	950		960
Tyr	Lys	Asp	Val	Phe	Ser	Tyr	Leu	Pro	Thr	Asp	Asn	Lys	Val	Leu	Met	965	970		975
Ala	Asp	Leu	Met	Phe	Arg	Lys	Gln	Lys	His	Glu	Ala	Ala	Ile	Asn	Leu	980	985		990
Tyr	His	Gln	Val	Leu	Glu	Lys	Ala	Pro	Gly	Asp	Asn	Phe	Leu	Val	Leu	995	1000		1005
His	Lys	Leu	Ile	Asp	Leu	Leu	Arg	Arg	Ser	Gly	Lys	Leu	Glu	Asp	Ile	1010	1015		1020
Pro	Ala	Phe	Phe	Glu	Leu	Ala	Lys	Lys	Val	Ser	Ser	Arg	Val	Pro	Leu	1025	1030		1040
Glu	Pro	Gly	Phe	Asn	Tyr	Cys	Arg	Gly	Ile	Tyr	Cys	Trp	His	Ile	Gly	1045	1050		1055
Gln	Pro	Asn	Glu	Ala	Leu	Lys	Phe	Leu	Asn	Lys	Ala	Arg	Lys	Asp	Ser	1060	1065		1070
Thr	Trp	Gly	Gln	Ser	Ala	Ile	Tyr	His	Met	Val	Gln	Ile	Cys	Leu	Asn	1075	1080		1085
Pro	Asp	Asn	Glu	Val	Val	Gly	Gly	Glu	Ala	Phe	Glu	Asn	Leu	Ile	Pro	1090	1095		1100
Arg	Ser	Asn	Thr	Cys	Ser	Tyr	Met	Glu	Lys	Lys	Glu	Leu	Glu	Gln	Gln	1105	1110		1120
Gly	Val	Ser	Thr	Ala	Glu	Lys	Leu	Leu	Arg	Glu	Phe	Tyr	Pro	His	Ser	1125	1130		1135
Asp	Ser	Ser	Gln	Thr	Gln	Leu	Arg	Leu	Leu	Gln	Gly	Leu	Cys	Arg	Leu	1140	1145		1150
Ala	Thr	Arg	Glu	Lys	Ala	Asn	Met	Glu	Ala	Ala	Leu	Gly	Ser	Phe	Ile	1155	1160		1165
Gln	Ile	Ala	Gln	Ala	Glu	Lys	Asp	Ser	Val	Pro	Ala	Leu	Leu	Ala	Leu	1170	1175		1180
Ala	Gln	Ala	Tyr	Val	Phe	Leu	Lys	Gln	Ile	Pro	Lys	Ala	Arg	Met	Gln	1185	1190		1200
Leu	Lys	Arg	Leu	Ala	Lys	Thr	Pro	Trp	Val	Leu	Ser	Glu	Ala	Glu	Asp	1205	1210		1215
Leu	Glu	Lys	Ser	Trp	Leu	Leu	Leu	Ala	Asp	Ile	Tyr	Cys	Gln	Gly	Ser	1220	1225		1230

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Ala	Ser	Glu	Gly 20	Ile	Lys	Arg	Tyr	Gly 25	Ser	Asp	Pro	Val	Phe 30	Arg	Phe
Tyr	His	Ala 35	Tyr	Gly	Thr	Leu	Met 40	Glu	Gly	Lys	Thr	Gln 45	Glu	Ala	Leu
Arg	Glu 50	Phe	Glu	Ala	Ile	Lys 55	Asn	Lys	Gln	Asp	Val 60	Ser	Leu	Cys	Ser
Leu 65	Leu	Ala	Leu	Ile	Tyr 70	Ala	His	Lys	Asp	Arg 75	Glu	Ala	Ile	Leu	Glu 80
Ser	Asp	Ala	Arg	Val 85	Lys	Glu	Gln	Arg	Lys 90	Gly	Ala	Gly	Glu 95	Lys	Ala
Leu	Tyr	His 100	Ala	Gly	Leu	Phe	Leu	Trp 105	His	Ile	Gly	Arg 110	His	Asp	Lys
Ala	Arg	Glu 115	Tyr	Ile	Asp	Arg	Met 120	Ile	Lys	Ile	Ser	Asp 125	Gly	Ser	Lys
Gln 130	Gly	His	Val	Leu	Lys	Ala 135	Trp	Leu	Asp	Ile	Thr 140	Arg	Gly	Lys	Glu
Pro 145	Tyr	Thr	Lys	Lys 150	Ala	Leu	Lys	Tyr	Phe 155	Glu	Glu	Gly	Leu 160	Gln	Asp 165
Gly	Asn	Asp	Thr	Phe 165	Ala	Leu	Leu	Gly	Lys 170	Val	Ser	Trp	Arg 175	Gln	Asn
Tyr	Ser	Gly 180	Ala	Leu	Glu	Thr	Val	Asn 185	Gln	Ile	Ile	Val	Asn 190	Phe	Pro
Ser	Phe 195	Leu	Pro	Ala	Phe	Val	Lys 200	Lys	Met	Lys	Leu	Gln 205	Leu	Ala	Leu
Gln 210	Asp	Trp	Asp	Gln	Thr	Val 215	Glu	Thr	Ala	Gln	Arg 220	Leu	Ser	Asn	Lys
Ile 225	Ile	Phe	Phe	Ser 230	Phe	Cys	Gly	Arg	Ser 235	Gln	Leu	Ile	Leu 240	Gln	Lys

Ile	Gln	Thr	Leu	Leu	Glu	Arg	Ala	Phe	Ser	Leu	Asn	Pro	Gln	Gln	Ser	
				245					250					255		
Glu	Phe	Ala	Thr	Glu	Leu	Gly	Tyr	Gln	Met	Ile	Leu	Gln	Gly	Arg	Val	
			260					265					270			
Lys	Glu	Ala	Leu	Lys	Trp	Tyr	Lys	Thr	Ala	Met	Thr	Leu	Asp	Glu	Thr	
		275					280					285				
Ser	Val	Ser	Ala	Leu	Val	Gly	Phe	Ile	Gln	Cys	Gln	Leu	Ile	Glu	Gly	
	290					295				300						
Gln	Leu	Gln	Asp	Ala	Asp	Gln	Gln	Leu	Glu	Phe	Leu	Asn	Glu	Ile	Gln	
305					310					315					320	
Gln	Ser	Ile	Gly	Lys	Ser	Ala	Val	Leu	Ile	Tyr	Leu	His	Ala	Val	Leu	
				325					330					335		
Ala	Met	Lys	Lys	Asn	Lys	Arg	Gln	Glu	Glu	Val	Ile	Asn	Leu	Leu	Asn	
			340					345					350			
Asp	Val	Leu	Asp	Thr	His	Phe	Ser	Gln	Leu	Glu	Gly	Leu	Pro	Leu	Gly	
		355					360					365				
Ile	Gln	Tyr	Phe	Glu	Lys	Leu	Asn	Pro	Asp	Phe	Leu	Leu	Glu	Ile	Val	
		370				375					380					
Met	Glu	Tyr	Leu	Ser	Phe	Cys	Pro	Met	Gln	Val	Ser	Asn	Tyr	Gly	Phe	
385					390					395					400	
Leu	Leu	Gly	Asp	Ile	Glu	Ala	Ala	Phe	Asn	Asn	Leu	Gln	His	Cys	Leu	
				405				410						415		
Glu	His	Asn	Pro	Ser	Tyr	Ala	Asp	Ala	His	Leu	Leu	Leu	Ala	Gln	Val	
			420				425						430			
Tyr	Leu	Ser	Gln	Glu	Lys	Val	Lys	Leu	Cys	Ser	Gln	Ser	Leu	Glu	Leu	
		435					440					445				
Cys	Leu	Ser	Tyr	Asp	Phe	Lys	Val	Gln	Val	Arg	Asp	Tyr	Pro	Leu	Tyr	
	450					455					460					
His	Leu	Ile	Lys	Ala	Gln	Ser	Gln	Lys	Lys	Met	Gly	Glu	Ile	Ala	Asp	
465					470					475					480	
Ala	Ile	Lys	Thr	Leu	His	Met	Ala	Met	Ser	Leu	Pro	Gly	Met	Lys	Arg	
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Ile	Gly	Ala	Ser	Thr	Lys	Ser	Lys	Asp	Arg	Lys	Thr	Glu	Val	Asp	Thr	
			500					505					510			
Ser	His	Arg	Leu	Ser	Ile	Phe	Leu	Glu	Leu	Ile	Asp	Val	His	Arg	Leu	
		515					520					525				
Asn	Gly	Glu	His	Glu	Ala	Thr	Lys	Val	Leu	Gln	Asp	Ala	Ile	His	Glu	
	530					535					540					
Phe	Ser	Gly	Thr	Ser	Glu	Glu	Val	Arg	Val	Thr	Ile	Ala	Asn	Ala	Asp	
545					550					555					560	
Leu	Ala	Leu	Ala	Gln	Gly	Asp	Ile	Glu	Arg	Ala	Leu	Ser	Ile	Leu	Gln	
				565				570						575		
Asn	Val	Thr	Ala	Glu	Gln	Pro	Tyr	Phe	Ile	Glu	Ala	Arg	Glu	Lys	Met	
			580					585					590			
Ala	Asp	Ile	Tyr	Leu	Lys	His	Arg	Lys	Asp	Lys	Met	Leu	Tyr	Ile	Thr	
		595					600					605				
Cys	Phe	Ala	Ile	Thr	Tyr	Tyr	Glu	Ala	Ala	Leu	Lys	Thr	Gly	Gln	Lys	
	610					615					620					
Asn	Tyr	Leu	Cys	Tyr	Asp	Leu	Ala	Glu	Leu	Leu	Leu	Lys	Leu	Lys	Trp	
625					630					635					640	
Tyr	Asp	Lys	Ala	Glu	Lys	Val	Leu	Gln	His	Ala	Leu	Ala	His	Glu	Pro	
				645					650					655		
Gly	Met	Lys	Ala	Arg	Glu	Leu	Gln	Ala	Arg	Val	Leu	Lys	Arg	Val	Gln	
			660					665					670			
Met	Glu	Gln	Pro	Asp	Ala	Val	Pro	Ala	Gln	Lys	His	Leu	Ala	Ala	Glu	
		675					680					685				

Ile	Cys	Ala	Glu	Ile	Ala	Lys	His	Ser	Val	Ala	Gln	Arg	Asp	Tyr	Glu
690						695					700				
Lys	Ala	Ile	Lys	Phe	Tyr	Arg	Glu	Ala	Leu	Val	His	Cys	Glu	Thr	Asp
705					710					715					720
Asn	Lys	Val	Asp	Asn	Tyr	Met	Thr	Leu	Ser	Arg	Leu	Ile	Asp	Leu	Leu
				725					730					735	
Arg	Arg	Cys	Gly	Lys	Leu	Glu	Asp	Val	Pro	Arg	Phe	Phe	Ser	Met	Ala
			740					745					750		
Glu	Lys	Arg	Asn	Ser	Arg	Ala	Lys	Leu	Glu	Pro	Gly	Phe	Gln	Tyr	Cys
		755					760					765			
Lys	Gly	Leu	Tyr	Leu	Trp	Tyr	Thr	Gly	Glu	Pro	Asn	Asp	Ala	Leu	Arg
	770					775					780				
His	Phe	Asn	Lys	Ala	Arg	Lys	Asp	Arg	Asp	Trp	Gly	Gln	Asn	Ala	Leu
785					790					795					800
Tyr	Asn	Met	Ile	Glu	Ile	Cys	Leu	Asn	Pro	Asp	Asn	Glu	Thr	Val	Gly
			805						810					815	
Gly	Glu	Val	Phe	Glu	Asn	Leu	Asp	Gly	Asp	Ser	Asn	Ser	Thr	Glu	Lys
			820					825					830		
Gln	Glu	Ser	Val	Gln	Leu	Ala	Val	Arg	Thr	Ala	Glu	Lys	Leu	Leu	Lys
		835					840					845			
Glu	Leu	Lys	Pro	Gln	Thr	Val	Gln	Gly	His	Val	Gln	Leu	Arg	Ile	Met
	850					855					860				
Glu	Asn	Tyr	Cys	Leu	Met	Ala	Thr	Lys	Gln	Lys	Ser	Asn	Val	Glu	Gln
865					870					875					880
Ala	Leu	Asn	Thr	Phe	Thr	Glu	Ile	Ala	Ala	Ser	Glu	Lys	Glu	His	Ile
				885					890					895	
Pro	Ala	Leu	Leu	Gly	Met	Ala	Thr	Ala	Tyr	Met	Ile	Leu	Lys	Gln	Thr
		900						905					910		
Pro	Arg	Ala	Arg	Asn	Gln	Leu	Lys	Arg	Ile	Ala	Lys	Met	Asn	Trp	Asn
		915					920					925			
Ala	Ile	Asp	Ala	Glu	Glu	Phe	Glu	Lys	Ser	Trp	Leu	Leu	Leu	Ala	Asp
	930					935					940				
Ile	Tyr	Ile	Gln	Ser	Ala	Lys	Tyr	Asp	Met	Ala	Glu	Asp	Leu	Leu	Lys
945					950					955					960
Arg	Cys	Leu	Arg	His	Asn	Arg	Ser	Cys	Cys	Lys	Ala	Tyr	Glu	Tyr	Met
				965					970					975	
Gly	Tyr	Ile	Met	Glu	Lys	Glu	Gln	Ala	Tyr	Thr	Asp	Ala	Ala	Leu	Asn
			980					985					990		
Tyr	Glu	Met	Ala	Trp	Lys	Tyr	Ser	Asn	Arg	Thr	Asn	Pro	Ala	Val	Gly
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<210> 40

<211> 1115

<212> PRT

<213> Caenorhabditis elegans

<400> 40

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Pro	Gly	His	Ile	Glu	Lys	Ala	Lys	Ala	Ser	Ile	Met	Met	Lys	Asp	Trp
			20					25					30		
Arg	Gly	Val	Met	Asp	Cys	Ile	Met	Asn	Ala	Asp	Gln	Pro	Glu	Gly	Ser
			35				40					45			
Asn	Pro	Tyr	Ile	Glu	Val	Leu	Arg	Thr	Val	His	Gly	Ile	Cys	Tyr	Ala
	50					55					60				
Gly	Glu	Val	Ser	Met	Leu	Lys	Arg	Thr	Leu	Gln	Leu	Leu	Leu	Lys	Ser
65					70					75					80

Leu	Asp	Glu	Asn	Glu	Ala	Thr	Asn	His	Val	Leu	Tyr	Ala	Arg	Ile	Thr
				85					90					95	
Lys	Leu	Leu	Val	Ser	Ile	Ser	Gly	Arg	Asp	Glu	Lys	Ile	Leu	Arg	His
			100					105					110		
Ala	Arg	Asp	Phe	Leu	Thr	Arg	Ala	Leu	Lys	Ile	Ser	Arg	Lys	Pro	Asp
		115					120					125			
Tyr	Val	Ala	Leu	Ser	Met	Arg	Ile	Ala	Phe	Gly	Leu	Gly	Gly	Ala	Lys
	130					135					140				
Glu	Val	Ser	Thr	Leu	Ser	Gln	Glu	Leu	Val	Ala	Leu	Asp	Cys	Glu	Asp
145					150					155				160	
Ser	Tyr	Ala	Val	Leu	Ser	Ser	Val	Val	Ser	Met	Leu	Met	Ile	Ser	Arg
			165						170					175	
Val	Ser	Asp	Ala	Arg	Ala	Gln	Phe	Asp	Ile	Leu	Pro	Ser	Ala	His	Pro
			180					185					190		
Lys	Leu	Leu	Glu	Ser	Pro	Leu	Tyr	Tyr	Leu	Ile	Ala	Ser	Val	Leu	Ala
		195					200					205			
Lys	Gln	Ser	Lys	Asp	Lys	Ser	Phe	Glu	Asn	Phe	Arg	Gln	His	Ile	Glu
	210					215					220				
Asn	Leu	Val	Glu	Met	Leu	Arg	Asn	Gln	Leu	Gln	Ser	Phe	Pro	Phe	Gly
225					230					235					240
Leu	Asp	Tyr	Leu	Ser	Leu	Phe	Ser	Ser	Asp	Leu	Leu	Tyr	Ser	Ala	Val
				245					250					255	
Glu	Gln	Cys	Phe	Asp	Phe	Tyr	Pro	Leu	Val	Pro	Ile	Lys	Ala	Pro	Asp
			260					265					270		
Asp	Cys	Met	Lys	Leu	Thr	Ala	Lys	Thr	Leu	Gln	Met	Ile	Tyr	Asp	Val
		275					280					285			
Ala	Pro	Gly	Leu	Ala	His	Cys	Thr	Leu	Gln	Leu	Ala	Arg	Asn	Ser	Tyr
		290				295					300				
Leu	Cys	Ser	Asn	Thr	Asn	Ala	Ala	Glu	Lys	Trp	Ile	Glu	Lys	Val	Leu
305					310					315					320
Asp	Lys	Asp	Asp	Ser	Leu	Ala	Asp	Ala	His	Ile	Leu	Arg	Ala	Glu	Leu
				325					330					335	
Ile	Leu	Asp	Arg	Gly	Gly	Lys	Ile	Thr	Asp	Ala	Asp	Asp	Ala	Leu	Val
			340					345					350		
Thr	Gly	Leu	Asn	Phe	Asn	Phe	Lys	Leu	Arg	Glu	Thr	Ser	Leu	Tyr	His
		355					360					365			
Leu	Ile	Lys	Ser	Lys	Thr	Phe	Lys	Lys	Arg	Asn	Glu	Asn	Asp	Glu	Ala
	370					375					380				
Ile	Lys	Thr	Leu	Lys	Met	Ala	Leu	Gln	Ile	Pro	Arg	Lys	Glu	Pro	Ser
385					390					395				400	
Lys	Asn	Leu	Phe	Gln	Pro	Lys	Glu	Ser	Ala	Asp	Thr	His	Lys	Ile	Ser
				405					410					415	
Val	Gln	Leu	Glu	Leu	Ile	Asp	Thr	Leu	Gln	His	Met	Lys	Arg	Ile	Gln
			420					425					430		
Glu	Ala	Glu	Thr	Thr	Met	Thr	Asp	Ala	Leu	Ala	Glu	Trp	Ala	Gly	Gln
		435					440					445			
Pro	Glu	Gln	Asp	Gln	Leu	Val	Ile	Ala	Gln	Ala	Gln	Leu	Tyr	Leu	Thr
		450				455					460				
Lys	Gly	His	Val	Glu	Arg	Ala	Leu	Gly	Ile	Leu	Lys	Lys	Ile	Gln	Pro
465					470					475				480	
Gly	Gln	Ser	Asn	Phe	His	Leu	Ser	Arg	Ile	Lys	Met	Ala	Glu	Ile	Tyr
				485					490					495	
Leu	Glu	Glu	Lys	Lys	Asp	Lys	Arg	Met	Phe	Ala	Ala	Cys	Tyr	Arg	Glu
			500					505					510		
Leu	Leu	Lys	Val	Glu	Ala	Thr	Pro	Gly	Ser	Tyr	Ser	Leu	Leu	Gly	Asp
		515					520					525			

Ala	Phe	Met	Lys	Val	Gln	Glu	Pro	Glu	Asp	Ala	Ile	Asn	Phe	Tyr	Glu
530						535					540				
Gln	Ala	Leu	Lys	Met	Gln	Ser	Lys	Asp	Val	Gln	Leu	Ala	Glu	Lys	Ile
545					550					555					560
Gly	Glu	Ala	Tyr	Val	Met	Ala	His	Leu	Tyr	Ser	Lys	Ala	Val	Asn	Phe
				565					570					575	
Tyr	Glu	Ser	Ser	Met	Asn	Ile	Tyr	Lys	Asp	Lys	Asn	Met	Arg	Leu	Lys
			580					585					590		
Leu	Ala	Asn	Leu	Leu	Leu	Lys	Leu	Arg	Asn	Phe	Glu	Lys	Cys	Glu	Lys
		595					600					605			
Val	Leu	Arg	Ala	Pro	Phe	Glu	Arg	Asp	Pro	Glu	Pro	Val	Gly	Thr	Glu
610						615					620				
Thr	Ile	Gln	Thr	Tyr	Ile	Gln	Phe	Leu	Leu	Leu	Leu	Ala	Glu	Cys	His
625					630					635					640
Glu	Met	Met	Asp	Asn	Val	Pro	Glu	Ala	Met	Asn	Asp	Phe	Glu	Lys	Ala
				645					650					655	
Lys	Ser	Leu	His	Ser	Arg	Ile	Gln	Asp	Lys	Thr	Leu	Thr	Ala	Ala	Leu
			660					665					670		
Lys	Lys	Glu	Gly	Ala	Arg	Ile	Cys	Asn	Leu	Gln	Ala	Glu	Leu	Leu	Tyr
		675					680					685			
Arg	Arg	Arg	Glu	Phe	Ser	Gln	Ala	Val	Asp	Ile	Cys	Lys	Gln	Ala	Leu
690					695					700					
Ala	Tyr	His	Glu	Thr	Asp	Leu	Lys	Ala	Asn	Leu	Leu	Leu	Ser	Lys	Ile
705					710					715					720
Phe	Lys	Glu	Glu	Asn	Lys	Trp	Thr	Leu	Val	Leu	Gln	Pro	Cys	Gln	Thr
				725					730					735	
Val	Ile	Gln	Val	Asp	Pro	His	Asn	Asp	Glu	Ala	Asn	Ser	Ile	Leu	Ala
			740					745					750		
Asp	Phe	Tyr	Tyr	Ile	Arg	Ser	Glu	Ala	Ala	His	Ala	Ser	Thr	Ser	Tyr
		755					760					765			
Thr	Thr	Leu	Leu	Asn	Thr	Asn	Pro	Gln	His	Trp	His	Ala	Leu	Ser	Arg
770					775					780					
Val	Val	Glu	Leu	Phe	Cys	Arg	Asn	Gly	Glu	Gln	Asn	Ala	Ala	Glu	Lys
785					790					795					800
His	Leu	Asp	Arg	Ala	Lys	Glu	Val	Asn	Pro	Arg	Cys	Val	Thr	Glu	Ser
				805					810					815	
Gly	Tyr	Asn	Val	Cys	Arg	Gly	Arg	Phe	Glu	Trp	Tyr	Thr	Gly	Asp	Gln
			820					825					830		
Asn	Glu	Ala	Leu	Arg	Tyr	Tyr	Ser	Arg	Thr	Lys	Asp	Ser	Ala	Ala	Gly
		835					840					845			
Trp	Arg	Glu	Lys	Ala	Leu	Tyr	Tyr	Met	Ile	Asp	Ile	Cys	Leu	Asn	Pro
850					855						860				
Asp	Asn	Glu	Ile	Ile	Ile	Asp	Glu	Asn	Ser	Val	Glu	Asn	Pro	Glu	Thr
865					870					875					880
Thr	Lys	Ile	Ile	Tyr	Leu	Val	Ser	Glu	Leu	Trp	Lys	Lys	Leu	Val	Asn
				885					890					895	
Ser	Lys	Asn	Leu	Pro	Asn	Ile	Thr	Ser	Ile	Tyr	Ser	Glu	Asn	Phe	Gln
			900					905					910		
Ser	Thr	Asp	Arg	Phe	Leu	Leu	Ala	Gln	Asn	Phe	Ile	Arg	Met	His	Thr
		915					920					925			
Thr	Asp	Lys	Ser	Ala	Ile	Gln	Ala	Ala	Leu	Asp	Glu	Phe	Asn	Arg	Met
930					935						940				
Ala	Phe	Asn	Ala	Asp	Arg	Ser	Gln	Val	Thr	Asn	Val	Gly	Ala	Val	Phe
945					950					955					960
Gly	Val	Ala	Arg	Gly	His	Val	Leu	Leu	Lys	Gln	Val	Gln	Lys	Ala	Lys
				965					970					975	

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Thr Val Leu Lys Met Val Asn Gly Arg Val Trp Asn Phe Asp Asp Ser
    980                      985                      990
Asp Tyr Leu Glu Lys Cys Trp Leu Met Leu Ala Asp Ile Tyr Ile Asn
    995                      1000                      1005
Gln Asn Lys Asn Asp Gln Ala Val Thr Phe Leu Asp Leu Val Phe Lys
    1010                      1015                      1020
Tyr Asn Cys Asn Cys Leu Lys Ala Phe Glu Leu Tyr Gly Tyr Met Arg
    1025                      1030                      1035                      1040
Glu Lys Glu Gln Lys Tyr Val Glu Ala Tyr Lys Met Tyr Glu Lys Ala
    1045                      1050                      1055
Phe Met Ala Thr Lys Glu Arg Asn Pro Gly Phe Gly Tyr Lys Leu Ala
    1060                      1065                      1070
Phe Thr Tyr Leu Lys Ala Lys Arg Leu Phe Ala Cys Ile Glu Thr Cys
    1075                      1080                      1085
Gln Lys Val Leu Asp Leu Asn Pro Gln Tyr Pro Lys Ile Lys Lys Glu
    1090                      1095                      1100
Ile Met Asp Lys Ala Lys Ala Leu Ile Arg Thr
    1105                      1110                      1115

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<210> 41
<211> 764
<212> PRT
<213> Homo sapiens

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<400> 41
Ile Glu Leu Val Ser Cys Val Gly Trp Thr Thr Ala Glu Glu Leu Tyr
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Ser Cys Ser Asp Asp His Gln Ile Val Lys Trp Asn Leu Leu Thr Ser
    20          25          30
Glu Thr Thr Gln Ile Val Lys Leu Pro Asp Asp Ile Tyr Pro Ile Asp
    35          40          45
Phe His Trp Phe Pro Lys Ser Leu Gly Val Lys Lys Gln Thr Gln Ala
    50          55          60
Glu Ser Phe Val Leu Thr Ser Ser Asp Gly Lys Phe His Leu Ile Ser
    65          70          75          80
Lys Leu Gly Arg Val Glu Lys Ser Val Glu Ala His Cys Gly Ala Val
    85          90          95
Leu Ala Gly Arg Trp Asn Tyr Glu Gly Thr Ala Leu Val Thr Val Gly
    100          105          110
Glu Asp Gly Gln Ile Lys Ile Trp Ser Lys Thr Gly Met Leu Arg Ser
    115          120          125
Thr Leu Ala Gln Gln Gly Thr Pro Val Tyr Ser Val Ala Trp Gly Pro
    130          135          140
Asp Ser Glu Lys Val Leu Tyr Thr Ala Gly Lys Gln Leu Ile Ile Lys
    145          150          155          160
Pro Leu Gln Pro Asn Ala Lys Val Leu Gln Trp Lys Ala His Asp Gly
    165          170          175
Ile Ile Leu Lys Val Asp Trp Asn Ser Val Asn Asp Leu Ile Leu Ser
    180          185          190
Ala Gly Glu Asp Cys Lys Tyr Lys Val Trp Asp Ser Tyr Gly Arg Pro
    195          200          205
Leu Tyr Asn Ser Gln Pro His Glu His Pro Ile Thr Ser Val Ala Trp
    210          215          220
Ala Pro Asp Gly Glu Leu Phe Ala Val Gly Ser Phe His Thr Leu Arg
    225          230          235          240
Leu Cys Asp Lys Thr Gly Trp Ser Tyr Ala Leu Glu Lys Pro Asn Thr
    245          250          255

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Gly Ser Ile Phe Asn Ile Ala Trp Ser Ile Asp Gly Thr Gln Ile Ala
 260 265 270
 Gly Ala Cys Gly Asn Gly His Val Val Phe Ala His Val Val Glu Gln
 275 280 285
 His Trp Glu Trp Lys Asn Phe Gln Val Thr Leu Thr Lys Arg Arg Ala
 290 295 300
 Met Gln Val Arg Asn Val Leu Asn Asp Ala Val Asp Leu Leu Glu Phe
 305 310 315 320
 Arg Asp Arg Val Ile Lys Ala Ser Leu Asn Tyr Ala His Leu Val Val
 325 330 335
 Ser Thr Ser Leu Gln Cys Tyr Val Phe Ser Thr Lys Asn Trp Asn Thr
 340 345 350
 Pro Ile Ile Phe Asp Leu Lys Glu Gly Thr Val Ser Leu Ile Leu Gln
 355 360 365
 Ala Glu Arg His Phe Leu Leu Val Asp Gly Ser Ser Ile Tyr Leu Tyr
 370 375 380
 Ser Tyr Glu Gly Arg Phe Ile Ser Ser Pro Lys Phe Pro Gly Met Arg
 385 390 395 400
 Thr Asp Ile Leu Asn Ala Gln Thr Val Ser Leu Ser Asn Asp Thr Ile
 405 410 415
 Ala Ile Arg Asp Lys Ala Asp Glu Lys Ile Ile Phe Leu Phe Glu Ala
 420 425 430
 Ser Thr Gly Lys Pro Leu Gly Asp Gly Lys Phe Leu Ser His Lys Asn
 435 440 445
 Glu Ile Leu Glu Ile Ala Leu Asp Gln Lys Gly Leu Thr Asn Asp Arg
 450 455 460
 Lys Ile Ala Phe Ile Asp Lys Asn Arg Asp Leu Cys Ile Thr Ser Val
 465 470 475 480
 Lys Arg Phe Gly Lys Glu Glu Gln Ile Ile Lys Leu Gly Thr Met Val
 485 490 495
 His Thr Leu Ala Trp Asn Asp Thr Cys Asn Ile Leu Cys Gly Leu Gln
 500 505 510
 Asp Thr Arg Phe Ile Val Trp Tyr Tyr Pro Asn Thr Val Tyr Val Asp
 515 520 525
 Arg Asp Ile Leu Pro Lys Thr Leu Tyr Glu Arg Asp Ala Ser Glu Phe
 530 535 540
 Ser Lys Asn Pro His Ile Val Ser Phe Val Gly Asn Gln Val Thr Ile
 545 550 555 560
 Arg Arg Ala Asp Gly Ser Leu Val His Ile Ser Ile Thr Pro Tyr Pro
 565 570 575
 Ala Ile Leu His Glu Tyr Val Ser Ser Ser Lys Trp Glu Asp Ala Val
 580 585 590
 Arg Leu Cys Arg Phe Val Lys Glu Gln Thr Met Trp Ala Cys Leu Ala
 595 600 605
 Ala Met Ala Val Ala Asn Arg Asp Met Thr Thr Ala Glu Ile Ala Tyr
 610 615 620
 Ala Ala Ile Gly Glu Ile Asp Lys Val Gln Tyr Ile Asn Ser Ile Lys
 625 630 635 640
 Asn Leu Pro Ser Lys Glu Ser Lys Met Ala His Ile Leu Leu Phe Ser
 645 650 655
 Gly Asn Ile Gln Glu Ala Glu Ile Val Leu Leu Gln Ala Gly Leu Val
 660 665 670
 Tyr Gln Ala Ile Gln Ile Asn Ile Asn Leu Tyr Asn Trp Glu Arg Ala
 675 680 685
 Leu Glu Leu Ala Val Lys Tyr Lys Thr His Val Asp Thr Val Leu Ala
 690 695 700

Tyr	Arg	Gln	Lys	Phe	Leu	Glu	Thr	Phe	Gly	Lys	Gln	Glu	Thr	Asn	Lys
705					710					715					720
Arg	Tyr	Leu	His	Tyr	Ala	Glu	Gly	Leu	Gln	Ile	Asp	Trp	Glu	Lys	Ile
				725					730					735	
Lys	Ala	Lys	Ile	Glu	Met	Glu	Ile	Thr	Lys	Glu	Arg	Glu	Gln	Ser	Ser
			740					745					750		
Ser	Ser	Gln	Ser	Ser	Lys	Ser	Ile	Gly	Leu	Lys	Pro				
		755					760								

<210> 42

<211> 760

<212> PRT

<213> Caenorhabditis elegans

<400> 42

Met	Lys	Leu	Lys	Leu	Ser	Ala	Ser	Arg	Lys	Thr	Arg	His	Thr	Glu	Met
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Val	Cys	Gly	Val	Gly	Trp	Ile	Gly	Thr	Glu	Ala	Ile	Leu	Ser	Ala	Ala
			20					25					30		
Asp	Asp	His	Val	Phe	Leu	Leu	Thr	Asn	Thr	Ala	Thr	Asn	Glu	Ser	Gln
		35					40					45			
Gln	Ile	Leu	Asn	Met	Pro	Glu	Thr	Phe	Phe	Pro	Thr	Ser	Leu	His	Ile
	50					55					60				
Phe	Pro	Arg	Ser	Gln	Thr	Lys	Gly	Gly	Gln	Asn	Asp	Val	Phe	Ala	Val
65					70					75					80
Ser	Thr	Ser	Asp	Gly	Lys	Ile	Asn	Ile	Leu	Ser	Arg	Asn	Gly	Lys	Val
				85					90					95	
Glu	Asn	Met	Val	Asp	Ala	His	Asn	Gly	Ala	Ala	Leu	Cys	Ala	Arg	Trp
			100					105					110		
Asn	Ser	Asp	Gly	Thr	Gly	Leu	Leu	Ser	Ser	Gly	Glu	Asp	Gly	Phe	Val
		115					120					125			
Lys	Met	Trp	Ser	Arg	Ser	Gly	Met	Leu	Arg	Ser	Val	Leu	Ala	Gln	Phe
	130					135					140				
Ala	Thr	Ala	Val	Tyr	Cys	Val	Ala	Trp	Asp	Ser	Thr	Ser	Ser	Asn	Val
145					150					155					160
Leu	Tyr	Cys	Asn	Ala	Asp	His	Cys	Tyr	Ile	Lys	Ser	Leu	Lys	Met	Gln
			165						170					175	
Val	Ala	Pro	Ile	Lys	Trp	Lys	Ala	His	Asp	Gly	Ile	Ile	Leu	Cys	Cys
			180					185					190		
Asp	Trp	Asn	Pro	Thr	Ser	Asp	Leu	Ile	Val	Thr	Gly	Gly	Glu	Asp	Leu
		195					200					205			
Lys	Phe	Lys	Val	Trp	Asp	Gly	Phe	Gly	Gln	Ile	Leu	Phe	Asn	Ser	Ser
	210					215					220				
Val	His	Asp	Tyr	Pro	Ile	Thr	Ser	Ile	Ser	Trp	Asn	Thr	Asp	Gly	Thr
225					230					235					240
Leu	Phe	Ala	Val	Gly	Ser	His	Asn	Ile	Leu	Arg	Leu	Cys	Asp	Lys	Ser
				245					250					255	
Gly	Trp	Ser	His	Ser	Leu	Glu	Lys	Met	Asn	Ala	Gly	Ser	Val	Met	Ala
			260					265					270		
Leu	Ser	Trp	Ser	Pro	Asp	Gly	Thr	Gln	Leu	Ala	Val	Gly	Thr	Ala	Ala
		275					280						285		
Gly	Leu	Val	Phe	His	Ala	His	Ile	Ile	Asp	Lys	Arg	Leu	Thr	Tyr	Glu
	290					295					300				
Glu	Phe	Glu	Ile	Val	Gln	Thr	Gln	Lys	Thr	Val	Ile	Glu	Val	Arg	Asp
305					310					315					320
Val	Ser	Ser	Glu	Val	Ser	Arg	Glu	Thr	Leu	Glu	Thr	Lys	Glu	Arg	Ile
				325					330					335	

Ser	Lys	Ile	Ala	Ile	Leu	Tyr	Lys	Tyr	Leu	Ile	Val	Val	Thr	Ser	Ser
			340					345					350		
His	Ile	Tyr	Ile	Tyr	Ser	Ser	Lys	Asn	Trp	Asn	Thr	Pro	Thr	Met	Ile
		355					360					365			
Glu	Tyr	Asn	Glu	Arg	Thr	Val	Asn	Ile	Ile	Val	Gln	Cys	Glu	Lys	Ile
	370					375					380				
Phe	Leu	Val	Ser	Asp	Gly	Met	Thr	Ile	Thr	Ile	Phe	Thr	Tyr	Glu	Gly
385					390					395					400
Arg	Lys	Leu	Ile	Asn	Leu	Asn	Pro	Pro	Gly	Gln	Val	Met	Ala	Leu	Leu
			405						410					415	
Asp	Glu	Arg	Lys	Ile	Asp	Leu	Ala	Asn	Asp	Thr	Leu	Val	Val	Arg	Asp
			420					425					430		
Arg	Ala	Asp	Asn	Lys	Val	Leu	His	Phe	Phe	Asp	Pro	Thr	Thr	Gly	Lys
		435					440					445			
Ala	Gln	Gly	Asp	Gly	Asn	Leu	Lys	His	Glu	His	Asp	Ile	Val	Glu	Leu
	450					455					460				
Thr	Val	Asn	Gln	Cys	Gly	Pro	Leu	Asn	Asp	Arg	Asn	Val	Ala	Phe	Arg
465					470					475					480
Asp	Gln	Ile	Gly	Ala	Val	His	Ile	Ala	Met	Val	Lys	Thr	Phe	Gly	Val
			485						490					495	
Ser	Gln	Arg	Met	Val	Lys	Ile	Gly	Ser	Leu	Val	Glu	Gln	Leu	Val	Phe
			500					505					510		
Asn	Asp	Val	Thr	Asn	Met	Leu	Cys	Gly	Ile	Ser	Glu	Gly	Lys	Ile	Ala
		515					520					525			
Val	Trp	Pro	Leu	Pro	Asn	Val	Ala	Phe	His	Asp	Arg	Asn	Leu	Leu	Gln
	530					535					540				
Lys	Ser	Leu	Ile	Gln	Lys	Asn	Ile	Gly	Ser	Val	Gly	Lys	Phe	Pro	Gln
545					550					555					560
Leu	Ala	Asn	Phe	Ala	Gly	Asn	Thr	Ile	Val	Ile	Arg	Lys	Ser	Asp	Gly
			565						570					575	
Cys	Leu	Leu	Pro	Thr	Gly	Ile	Leu	Pro	Phe	Tyr	Gly	Thr	Leu	Ile	Thr
			580					585					590		
Met	Ala	Ser	Gln	Ser	Lys	Trp	Asp	Gln	Ala	Ile	Arg	Leu	Cys	Arg	Ser
		595					600					605			
Ile	Gly	Asn	Asp	Thr	Met	Trp	Ala	Thr	Phe	Ala	Gly	Leu	Ala	Val	Leu
	610					615					620				
His	Lys	Asn	Met	Ile	Val	Met	Glu	Ile	Ala	Tyr	Ala	Ala	Leu	Glu	Asp
625					630					635					640
Asp	Glu	Lys	Val	Ser	Leu	Ile	Asn	Glu	Ile	Lys	Asp	Lys	Thr	Asp	Lys
			645						650					655	
Glu	Thr	Arg	Gln	Ala	Met	Gln	Val	Val	Leu	Thr	Gly	Lys	Leu	Ala	Asp
			660					665					670		
Ala	Asp	Val	Leu	Leu	Glu	Arg	Ser	Gly	Leu	Ser	Phe	Arg	Ser	Leu	Met
		675					680					685			
Leu															

<210> 43

<211> 8

<400> 48
Ser Leu Phe Asn Glu Ala Ala Gly Ile Asp Pro Tyr Cys Val Glu Ala
1 5 10 15


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<210> 49
<211> 11
<212> PRT
<213> Chlamydomonas reinhardtii
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<210> 50
<211> 11
<212> PRT
<213> Chlamydomonas reinhardtii
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<400> 50
Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg
1 5 10